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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 19:01:57 ; Search time 4798 Seconds
(without alignments)
11239.579 Million cell updates/sec

Title: US-09-977-221-2-C-AT-1513

Perfect score: 1853

Sequence: 1 aaaaagcaggaggaggct.....cgtctgtaatcccaacctttt 1853

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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9: gb_pr.*

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11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: en_ba.*

16: en_fun.*

17: en_hum.*

18: en_in.*

19: en_mu.*

20: en_om.*

21: en_or.*

22: en_ov.*

23: en_pat.*

24: en_ph.*

25: en_pl.*

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28: en_un.*

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30: en_hgt_hum.*

31: en_hgt_inv.*

32: en_hgt_other.*

33: en_hgt_mus.*

34: en_hgt_pln.*

35: en_hgt_rod.*

36: en_hgt_mam.*

37: en_hgt_vrt.*

38: en_sy.*

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40: en_hgt_mus.*

41: en_hgt_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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3	1843.8	99.5	1853	6	AR116693	AR116693 Sequence
4	1836.6	99.1	2164	9	BC011913	BC011913 Homo sapi
5	1835	99.0	2168	6	AX099420	AX099420 Sequence
6	1428	77.1	2011	9	AK090866	AK090866 Homo sapi
7	1281.2	69.1	3540	6	AR116692	AR116692 Sequence
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9	1269.6	68.5	1810	10	MMU9823	AJ009823 Mus muscu
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15	344.4	18.6	66872	2	AC115728	AC115728 Mus muscu
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ALIGNMENTS

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LOCUS AX427649 1853 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 2 from Patent EPI199372.
ACCESSION AX427649
VERSION AX427649.1 GI:21537769
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Morten,J.E.
TITLE Polymorphisms in the human p2x7 gene
JOURNAL Patent:EP 1199372-A 2 24-APR-2002;


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RESULT 6
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ACCESSION AK090866
VERSION 1 GI:21749107
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SOURCE Homo sapiens amygdala cDNA to mRNA, clone_lib:BRAMY2
Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tashiro, H., Yamazaki, M., Watanabe, K., Kunagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Negatani, K., Masuhara, Y., Negai, K. and Isogai, T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2011)
AUTHORS Isogai, T. and Yamamoto, J.
TITLE Direct Submision
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 252-0812, Japan (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

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VERSION	X95882.1	GI:1322004	
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AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
TITLE	Rattus.		
JOURNAL	1 (bases 1 to 3540)		
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PUBMED	The cytolytic P2Z receptor for extracellular ATP identified as a		
REFERENCE	P2X receptor (P2X7)		
AUTHORS	Science 272 (5262), 735-738 (1996)		
TITLE	96202420		
JOURNAL	8614837		
MEDLINE	2 (bases 1 to 3540)		
PUBMED	Buell,G.N.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (26-FEB-1996) G.N. Buell, Glaxo, Molecular Biology, 14		
TITLE	Chemin des Auxil, 1228 Plan-Ies-Ouates, Geneva, SWITZERLAND		
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VERSION     AJ009823.1 GI:4007637
KEYWORDS   P2X7 gene; P2X7 receptor subunit.
SOURCE      house mouse.
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REFERENCE   1 (bases 1 to 1810)
AUTHORS     Simon, J.
TITLE       Direct Submission
JOURNAL     Submitted (28-JUL-1998) Simon J., Department of Pharmacology,
            University of Cambridge, Glaxo Institute of Applied Pharmacology,
            Tennis Court Road, Cambridge, CB2 1QJ, UNITED KINGDOM
REFERENCE   2 (bases 1 to 1810)
AUTHORS     Chessell, I.P.; Simon, J.; Hibell, A.D.; Michel, A.D.; Barnard, E.A. and
            Humphrey, P.P.A.
TITLE       Cloning and functional characterisation of the mouse P2X7 receptor
JOURNAL     FEBS Lett. 4390, 260-300 (1998)
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QY      687 ACTCAGAACTCCACAGTGTCCCAATTTCCGACTAGGAGACATCTCCGAGAAACAGGAG 746
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QY      1227 GTGTCTTTGATGAATCCCACTTAGGATGGTGAACCAAGCAAGCTACTAGGAGAGT 1286
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QY      1347 AGGTGCGCCCTGCGCTTCCATGACACACCCCGCTTCCTGGACACCAAGAGATACRG 1406

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AUTHORS

Rattus.
1 (bases 1 to 115282)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Avele,M., Banks,T.,
Barbala,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Delava,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.B., Ding,Y., Dinh,H.H.,
Douchwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
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Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Homsí,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
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Karlssohn,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
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Li,J., Li,Z., Lichtarge,O., Lieu,C., Lucier,R., Luna,R., Ma,J.,
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Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
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Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
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Oreguene,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
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Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatka,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
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Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
Worley, K.C.
2 (bases 1 to 115282)
Direct Submission
Submitted (08-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHX
Center clone name: CH230-83K8
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 56769 bases at least Q40
Consensus quality: 59422 bases at least Q30
Consensus quality: 61794 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see <http://www.hgsc.bcm.tmc.edu/docs/Genbankdraft.data.html>).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 56 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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5210: gap of unknown length
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7669: gap of unknown length
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9479: gap of unknown length
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16572: contig of 1266 bp in length
16772: gap of unknown length
18124: contig of 1452 bp in length
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21563: contig of 1418 bp in length
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24324: contig of 1152 bp in length
24424: gap of unknown length
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39028: gap of unknown length
40222: contig of 1194 bp in length
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47752: contig of 1204 bp in length
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50099: gap of unknown length
51493: contig of 1394 bp in length
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55528: contig of 1985 bp in length
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* 70020 70120: gap of unknown length
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* 78559 80813: contig of 2255 bp in length
* 80814 80914: gap of unknown length
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* 83925 86080: contig of 2155 bp in length
* 86080 86179: gap of unknown length
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* 94532 97041: contig of 2410 bp in length
* 97042 97141: gap of unknown length
* 97142 99551: contig of 2810 bp in length
* 99552 100511: gap of unknown length
* 100512 103222: contig of 3171 bp in length
* 103223 103322: gap of unknown length
* 103323 107840: contig of 4518 bp in length
* 107841 107940: gap of unknown length
* 107941 110756: contig of 2816 bp in length
* 110757 110856: gap of unknown length
* 110857 115282: contig of 4426 bp in length.
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            /organism="Rattus norvegicus"
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Best Local Similarity 80.5%; Pred. No. 1.8e-78;
Matches 405; Conservative 3; Mismatches 95; Indels 0; Gaps 0;
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DB 105405 TTACAGACCCAGCAGCAGACTCTTGGAAGTCTAGGCTCTCCCTCTCCACACT 105346
QY 1372 CACCCCGAGTCTCTGGACAACACAGAGAGATACRGCTGCTTAGAAGAGCGGACTCCTA 1431
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QY 1432 GATCCAGGATAGCCCTGCTGCTGGAGCTGTGGAGCTGCTCCATCTCACTCCCTG 1491
DB 105285 GGTCCAGGAGACGCCAGATTTGGTGCAGTGTGGAACTGCTCCCTGCTCACTCCAG 105226
QY 1492 AGGCCCAAGTGTCTGGAGCGCTGTGCTGCCGGAAGAAAGCCGGGCGCTGCTACCA 1551
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QY 1552 CCTCAGAGCTGTTCAGGAGCTGTCTGCTTCACAGACAGCTCTCGAGTTCTCTGCTCT 1611
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DB 105105 ACCAGAGCCCTGCTGCGCTGGAGGAGAGGAGCCATCAACAGCAAGCTGCGACACTGTG 105046

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DEFINITION Mus musculus clone RP23-37P22, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC117579
VERSION AC117579.2 GI:20976671
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
    1 (bases 1 to 66872)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
    Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
    Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
    Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
    Cook,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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    Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
    Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
    Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R.,
    Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
    Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
    McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
    Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
    Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
    Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
    Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
    Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,
    Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
    Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
    Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
    Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
    Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE
    3 (bases 1 to 66872)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
    Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
    Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
    Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
    Cook,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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    Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
    Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
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Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE JOURNAL

Submitted (18-MAY-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 18, 2002 this sequence version replaced gi:20128322.

COMMENT

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997).

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L23320

Center clone name: 37_P_22

* NOTE: This record contains 85 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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43259 43358: gap of 100 bp

43359 44043: contig of 685 bp in length

44044 44143: gap of 100 bp

44144 44842: contig of 697 bp in length

44843 14942: gap of 100 bp

14943 15631: contig of 689 bp in length

15632 15731: gap of 100 bp

15732 16424: contig of 693 bp in length

16425 16524: gap of 100 bp

Query Match 18.6%; Score 344.4; DB 2; Length 66872;
Best Local Similarity 79.4%; Pred.No. 4.2e-77;
Matches 405; Conservative 2; Mismatches 103; Indels 0; Gaps 0;


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QY 1312 TCCSAGACCTGYGATGACATTCACAGATTGTCCAGGCTGCCCTGGCCCTCCATGACA 1371
Db 38022 TTCAGAGACCCAGATGACATTCACAGATTGTCCAGGCTGCCCTGGCCCTCCATGACA 38081
QY 1372 CACCCCGGATTCTCTGGACACAGAGAGATACRGCTGTWAGAAAGGAGGCGACATCCA 1431
Db 38082 CACCCCTGACTCTCTGGACATCTGAGGAAATTCAGCTCTCCATGAGAGGTGGCCCTCA 38141
QY 1432 GATCCAGGATAGCCCTGCTGGTGGCCAGTGTGGAAGCTGCTCCCATCTCAACTCCCTG 1491
Db 38142 AGTCCGGGACAGCCCGAGTGTGGCCAGTGTGGAATTCGCTCCCTCTCGCTACCGG 38201
QY 1492 AGRCCACAGGTGCTGAGGCGCTGTGCTGCCGGAAGAAAGCCGGGGGCTGCAATCACA 1551
Db 38202 AGCAAGCCAGGCGCTGAGGAGCTGTGCTGCCGGAAGAAAGCCGGGGGCTGCAATCACA 38261
QY 1552 CCTCAGAGCTGTTCAGGAAGTGTGCTGTCCAGACAGCTGCTGAGTTCCTCTGCTCT 1611
Db 38262 CCTCCAGCTCTTCCATAGCTGTGCTGTCCGAGACACCTGTGAGCTCTCTCTCTTT 38321
QY 1612 ACCAGGAGCCCTGTGCTKCGGTGATGTGATTCACCAACAGCCGGCTCGGCACCTGTG 1671
Db 38322 ACCAGGATCCCTGTGCTGTGGGGAAGAGAGGCCACCAACAGCAGGCTCGACACCGTG 38381
QY 1672 CCTACAGGTGCTACGCCACCTGGCGCTTGGCTCCAGGACATGGCTGACTTTGCCATCC 1731
Db 38382 CTTACAGGTGCTATGCCACCTGGCGCTTGGCTTCCAGGACATGGCGACTTTGCCATTC 38441
QY 1732 TGCCAGCTGTGCGCTGGAGGATCGGGAAGAGTTCCRAAGAGTGAAGGGCAGTACA 1791
Db 38442 TGCCAGCTGTGCGCTGGAGGATCGGGAAGAGTTCGCCAGAGAGTTGCCAGAGGGCAGTATA 38501
QY 1792 GTGGCTCAAGAGTCCCTTACTGTAAGCCAGG 1821
Db 38502 GTGGCTCAAGTATCCCTACTGTATGTACG 38531
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Search completed: July 18, 2003, 22:13:47
Job time : 4809 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 19:00:18 ; Search time 446 Seconds
(without alignments)
9356.397 Million cell updates/sec

Title: US-09-977-221-2-C-AT-1513

Perfect score: 1853

Sequence: 1 aaacgcaggaggagagct.....cgtcgtgaatccccacatttt 1853

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_101002.*

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24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %	Score	Match	Length	ID	Description
1	1845.4	99.6	1853	24	AA43027	Human P2X7 gene co
2	1843.8	99.5	1853	22	AAC63694	Human P2X ₇ /P22 co
3	1835	99.0	2168	22	AAF9411	Human cDNA clone C
4	1832.2	98.9	2169	19	AAV30932	Human secreted pro
5	1261.2	69.1	3540	22	AAC63693	Rat P2X ₇ /P22 codi
6	237	12.8	1762	19	AAV27197	HPUR nucleic acid
7	235.4	12.7	1206	22	AAH25211	Nucleotide sequenc
8	235.4	12.7	1759	18	AAV09307	Human brain P2X-1
9	234.6	12.7	1997	17	AAT33853	Rat superior cervi

10	233.8	12.6	1207	22	AA404979	Human purinergic r
11	227.2	12.3	1807	18	AAV09308	Human brain P2X-2
12	203.8	11.0	2633	24	ABK84338	Human cDNA differe
13	203.8	11.0	2633	24	ABL70017	Pancreas cancer re
14	203.8	11.0	2643	17	AAT33855	Human urinary blad
15	196.4	10.6	294	20	AAV89619	EST clone CO390.
16	168.8	9.1	1784	23	AA576004	DNA encoding novel
17	159.6	8.6	1837	17	AAT33852	Rat vas deferens P
18	148.4	8.0	1272	20	AAH87357	Human P2X3 puriner
19	148.4	8.0	1272	21	AAC64099	Human P2X-3 recep
20	148.4	8.0	1272	22	AA404964	Human P2X3 cDNA 5'
21	148	8.0	1243	20	AAH87356	Human P2X3 puriner
22	148	8.0	1243	21	AAC64101	Human P2X-3 recep
23	148	8.0	1243	22	AA404966	Human purinergic r
24	147.4	8.0	4900	24	AA43026	Human P2X7 gene 5'
25	145.8	7.9	1272	22	AA404988	Human P2X3 cDNA 5'
26	142.6	7.7	11266	24	AA43028	Human P2X7 gene in
27	140.2	7.6	1753	17	AAT33854	Rat dorsal root ga
28	140	7.6	1421	21	AAZ51322	Human purino recep
29	140	7.6	1421	22	AAH25208	Nucleotide sequenc
30	140	7.6	1436	21	AAZ51321	Human purino recep
31	140	7.6	1436	22	AAH25207	Nucleotide sequenc
32	138.6	7.5	1240	22	AA404982	Human purinergic r
33	138.4	7.5	1349	21	AAZ51323	Human purino recep
34	138.4	7.5	1349	22	AAH25209	Nucleotide sequenc
35	138.2	7.5	1639	23	ABK43717	DNA encoding novel
36	135.6	7.3	1499	21	AAZ51324	Human purino recep
37	135.6	7.3	1499	22	AAH25210	Nucleotide sequenc
38	111.6	6.0	564	22	AA192047	Human polynucleoti
39	111	6.0	1697	19	AAV61833	Coding sequence fo
40	109.4	5.9	1293	19	AAV61832	Coding sequence fo
41	107.8	5.8	1360	22	AA404978	Human purinergic r
42	102.6	5.5	1956	24	ABK09794	Human ovarian tumo
43	102.6	5.5	1986	24	ABK84358	Human cDNA differe
44	101.2	5.5	1973	24	ABN59853	Novel human coding
45	96.8	5.2	878	15	AAQ73761	RP-2 Programmed ce

ALIGNMENTS

RESULT 1

AA43027	
ID	AA43027 standard; DNA; 1853 BP.
XX	
AC	AA43027;
XX	
DT	08-AUG-2002 (first entry)
XX	
DE	Human P2X7 gene coding sequence.
XX	
KW	Human; ds; single nucleotide polymorphism; SNP; P2X7-associated disorder;
KW	inflammation; immune disease; drug development; genetic marker; gene;
KW	P2X7 gene.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	27..1814
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FT	/product= "Human P2X7 protein"
FT	replace (253, C)
FT	/*tag= b
FT	/note= "Single nucleotide polymorphism"
FT	replace (488, A)
FT	/*tag= c
FT	/note= "Single nucleotide polymorphism"
FT	replace (489, T)
FT	/*tag= d
FT	/note= "Single nucleotide polymorphism"
FT	replace (760, G)
FT	/*tag= e
FT	/note= "Single nucleotide polymorphism"

Db 826 CCAGGAATCGGAGAGAACTTTACAGAGGTGGCCAGTTCCAGGAGGAATCATGGCAATGA 885
QY 791 GATCTACTGGGACTGCAACTAGACCGTTGCTTCATCACTGCGCTCCCAATACAGTTT 850
Db 886 GATCTACTGGGACTGCAACTGAGAGGTGGTCCCATCGCTGCTCAACCCAAATACAGTT 945
QY 851 CORTGCGCTTGACGACAAAGACACCAAGTGTCTTGTACCTGGCTCAACATTCAGATA 910
Db 946 CGCGCGGTGGAGCAAGTACACCAATGAGTCCCTGTTCCCTGGCTCAACATTCAGATA 1005
QY 911 GCCCAAGTACTACAGGAAGAAACAATGTTGGAAGACGAGCTCTCATAAAAGTCTTCGGAT 970
Db 1006 GCCCAAGTACTATAAAGGAAATGGCATGAGAAAGGAGCATTCATCAAGGCTTCGGGT 1065
QY 971 CGGTTTTCAGATCTGTTTGGCACCGGAGGAGAAATTTGACATTCATCCACTGGTGT 1030
Db 1066 CGGTTTTCAGATCTGTTTGGCACTGGAGGAGAAATTTGACATTCATCCACTGGTGT 1125
QY 1031 GTACATCGGCTCAACCTCTCCTACTCTGGTCTGGCCRCCTGTCTTCATCGACTTCCCTCAT 1090
Db 1126 GTACATTCGATCCACCTGTCTTATTCGGTTTGGCCACCGTGTGTATTCGACTTGATCAT 1185
QY 1091 CGACASTTACTCAGTACTGCTGCTGCCATATTTATCCCTGGTGAAGTGTGTCTCA 1150
Db 1186 CAACAGTATGCCAGTACTGCTGCGAGTCACTGTTTACCCCTCTCTGAAGTGTGCGA 1245
QY 1151 GCCCTGTGTGTCAACGATACTACTACAGGAAGTGGAGTCCATTTGTCGAGCCAAA 1210
Db 1246 GCCCTGTGTGTCAAGTACTACTACAGGAAGTGGAGTCCATTTGTCGAGCCAAA 1305
QY 1211 GCCGACATTAAGTATGTCCTTTGATGAATCCACATTTAGGATGGTGAACACGA 1270
Db 1306 GCCGACGTTAAGTATGTCCTTTGATGAAGTCCACATTTGATGGTGAACACGA 1365
QY 1271 GATCTAGGAGAGTCTGAGATGTCAAGGCTCAAGAGTCCSAGACCTGTGTATGGA 1330
Db 1366 GGTGTTGGGAAAAGTGTCAAGATGTCAAGGCTCAAGAGTCCGAGAGTCCGAGACCGCA 1425
QY 1331 CTTACAGATTTGCCAGGCTGCCCTGGCCCTCCATGACACACCCCGCATTCCTGGACA 1390
Db 1426 CTTCTGGAATGTCFAGGCTCTCCCTCTCTCCACACTCACCCCAATTCCTGGACA 1485
QY 1391 ACCAGAGGAGATACRGCTGTGTAGAAAGGCGGACCTCTAGATCCAGGATAGCCCTGT 1450
Db 1486 ACCTGAGGAATGCACTGTCTCCAGATAGAGGCTCTTAGTCCAGGACAGCCAGA 1545
QY 1451 CTGGTGCAGTGTGAGAGTCTCCATCTCACTCTCTGAGGCGCACAGTGTCTGGA 1510
Db 1546 TTGGTGCCAGTGTGGAAGTCTCCCTCCCTCTCAACTACAGAGAACCGAGGCGCTGGA 1605
QY 1511 GCGCTGTGTCGCGGAAAAGCGGGGCGCTGTGATCACCACCTCAGAGCTGTTCAGAA 1570
Db 1606 GAGTGTGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1665
QY 1571 GCTGTCTCTGTCACAGACGCTCTCTGAGTCTCTCTGATCTCTACAGAGGCTCTGCTG 1630
Db 1666 GATCTGTCTATCCAGAGGCGCTCTGAGTCTCTCTGATCTCTACAGAGGCTCTGCTG 1725
QY 1631 GCTGATGTGATTCACACAGCGGCTGCGGAGTCTGCTCTACAGTGTGATGCGCAC 1690
Db 1726 GCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1785
QY 1691 CTGGGCGCTTCGCGTCCAGAGACATGCTGACTTTGGCATCTCCAGGCTGTGCGCGT 1750
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QY 1751 GAGGATCCGGAAGAGTTTCCRAAGAGTGAAGGAGGAGTACAGTGGCTTCAAGAGTCTTA 1810
Db 1846 GAAGATCCGGAAGAGTTTCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1905
QY 1811 CTGA 1814
Db 1906 CTGA 1909

RESULT 6

AAV27197
ID AAV27197 standard; cDNA; 1762 BP.
XX AC AAV27197;
XX DT 28-SEP-1998 (first entry)
XX DE HPURR nucleic acid sequence.
XX KW Purinoreceptor; HPURR; P2x; rat; spinal cord; immune system;
XX KW nervous system; cardiovascular; smooth muscle; Alzheimer's; Huntington's
XX KW Parkinson's; Creutzfeldt-Jakob disease; thrombosis; ss.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT CDS 28..1554
XX FT /*tag= a
XX FT /product= "HPURR protein"
XX FI
XX FN WO9818916-A1.
XX PD 07-MAY-1998.
XX PF 15-OCT-1997; 97WO-US18370.
XX PR 30-OCT-1996; 96US-0742621.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Coleman R, Hillman JL;
XX DR WFI; 1998-272212/24.
DR P-PSDB; AAW55035.
XX PT Human purino-receptor and related nucleic acid - potentially useful
PT for diagnosing or treating immune, nervous system, cardiovascular
PT and smooth muscle diseases
XX Claim 5; Page 51-55; 66pp; English.
XX CC This nucleic acid sequence encodes the human purinoreceptor (HPURR),
XX which has been shown to be similar to P2x purinoreceptors isolated from
XX both human and rat. The nucleic acid was discovered from a spinal cord
XX DNA library (SCORNO01) Incyte clone 555697, this was found by using a
XX search for sequence alignments of amino acids. The consensus sequence
XX was derived from the two overlapping and/or extended nucleic acid
XX sequences: Incyte clones 555697 and 133269. These sequences can be used
XX in the diagnosis, prevention, and treatment of disorders and diseases of
XX the immune system, nervous system, cardiovascular, and of smooth muscle.
XX For example, Alzheimer's, Huntington's, Parkinson's, Creutzfeldt-Jakob
XX diseases, heart disease, stroke, thrombosis and other coagulation
XX disorders.
SQ Sequence 1762 BP; 399 A; 495 C; 481 G; 387 T; 0 other;
Query Match 12.8%; Score 237; DB 19; Length 1762;
Best Local Similarity 54.4%; Pred. No. 1.5e-54;
Matches 574; Conservative 5; Mismatches 440; Indels 36; Gaps 4;
QY 55 TTTTTCAGTATGACAGCAACAAAGTCACTCGGATCCAGAGCATGAATTTGGCACCATT 114
Db 62 TGTGTAGTAGAGACAGCCCGCGCATCTGCTCCGAGCCGCAAGATGGGCGCTCATGA 121
QY 115 AGTGTCTTCCAGTGCATCATCTTTCTTAG--TTTGTCTTGTCTGGTGAAGTACA 171
Db 122 ACCGCGCGTCAACTGCTCATCTGCGCTACGTCATCGGTGGGTGGTGTGGTGGAAA 181
QY 172 AGCTGTACAGCGGAAGAGCCCTGTCATCAGTCTGTGTGTCACACCAAGGTGAAGGGGATAG 231

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Db 182 AGGGCTACCGAARACTGACTCCGTGGTCACTCCGTTACGACCAAGGTCAGAGCGGTGG 241
Qy 232 CAGAGGTGAAGAGAGAGATCGYGGGAATGAGAGTGAAGAAGTTGGTGACAGTGTCTTTG 291
Db 242 CTGTGACCAACACTCTTAACATGGATCCGGATCTGGGATGTGGGATTAATGTGATAC 301
Qy 292 ACACGGCAGACTACACCTCCCTTGCAGGGGAACTCTTCTTCGFGAGACAACTTTC 351
Db 302 CAG-----CTCAGGAGGAARACTCCCTCTTCGTCATGACCAACGTGA 343
Qy 352 TCAAAACAGAGGCCAGAGACGCGGTTGTGTCCCGAGTATCCACCCCGACGACGTCT 411
Db 344 TCCTCACCATGAACACAGACAGGCGCTGTGCCCGGAGATTCAGATGGGACCACTGT 403
Qy 412 GTTCTCTGACCGAGGTGTAAAGAGGATGATGGACCCGACAGACGAAGAANTCAGA 471
Db 404 GTAATATCAGATGCCAGCTGTACTCGCGCTCTGCCGACCCACACGAACGAGGTCFAA 463
Qy 472 CCGGAAGTGTGTAGTATGAGGAGACCAAGAACCTGTGAAGTCTCTGCTGGTGCC 531
Db 464 CAGGAGGTGCTGTACTTTCACGCGTCCGTCAGAGCTGTGAGGTGGCGGCTGTGGCC 523
Qy 532 CCATCGAGGAGTGAAGAGGCCGCCCGGCTGTCTCTGAACAGTCCGCAAACTTCA 591
Db 524 CGGTGGAGGATGACACACAGCTGCCACAACTGTCTTTTAAAGGCTGCAGAAACTTCA 583
Qy 592 CTGTCTCATCAAGAACATATGACGTTCCCGGGCCAACTACACACGAGAAACATPC 651
Db 584 CTCCTTTGGTTAAGAACACATCTGGTATCCCAAAATTAATTTCAAGAGAGATATCC 643
Qy 652 TGCAGGTTTAAACATCACT-----TGTACTTCCCAAGACTCAGATCCAC 699
Db 644 TCCCAACATCAACACTACTTACTCAGTGTGCTGATTTATGATGAATAAACAGATCCCT 703
Qy 700 AATGTCATTTCCGACTAGGAGACATCTCCGAGAAACAGCGGATATTTTTCAGATG 759
Db 704 TCTGCCCATATTCCTGCTTGGCAAAATAGTGGAGACGCGAGACACATTTCCAGGACA 763
Qy 760 KGCATTCAGGGCGGATATGAGCATGTAGACTTACTGGGACTGCACTTACCTAGACGTT 819
Db 764 TGGCGGTGGAGGGAGGATCATGGGCATCCAGGTCAACTGGGACTGCACTTGGACAGAG 823
Qy 820 GGTTCATCACTGTCCTCCCAATACAGTTTCCTGCGCTTGACGACCAAGACCAACG 879
Db 824 CCGCTCCCTCTGCTCCGAGTACTCTTCGCGGCTCGATACAGGACGTTGAC 883
Qy 880 TGTCTTTGACCTGGCTACACTTCAGATAGCCGACGATCTACTACAAGGAAACAATG--- 936
Db 884 ACAAGGTATCTCTGGCTACATTTTCAGGTTTGGCAAGTACTACTACAGAGACCTGGTGCA 943
Qy 937 TTGAGAAACGGACTCTGATAAAAGTCTTCGGGATCCGTTTGTGACATCTCTGGTTTGGCA 996
Db 944 AGCAGCAGGACGCTCATCAGGCCATGGGATCCGGTTCGACATCATGTGTTTGGGA 1003
Qy 997 CCGAGAGAAATTTGACATTTACAGCTGGTGTGTATACATCGGCTCAACCCCTCTACT 1056
Db 1004 AGCAGGAGAAATTTGACATCATCCCACTATGATCAATCGGCTCTGGCTGGCAGTCG 1063
Qy 1057 TGGTCTGGCCCTGCTGTTTCACTGCACTTCTCAIC 1091
Db 1064 TAGGATGGCGACGCTGCTGTGATCATATAGTC 1098
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RESULT 7

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AAH25211
ID AAH25211 standard; DNA; 1206 BP.
XX
AC AAH25211;
XX
DT 22-AUG-2001 (first entry)
XX
DE Nucleotide sequence of a human purinoreceptor P2X4.
XX
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KW Human; purinoreceptor; P2X2; P2X4; pain; neuroendocrine disease;
KW auditory disease; vestibular disorder; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX CDS 21..1187
XX FT /*tag= a
XX FT /product= "purinoreceptor P2X4"
XX
XX US6242216-B1.
XX
XX PD 05-JUN-2001.
XX
XX PF 13-NOV-1998; 98US-0191608.
XX PR 14-NOV-1997; 97US-0065822.
XX PR 20-AUG-1998; 98US-0137458.
XX
XX PA (ABBO ) ABBOTT LAB.
XX
XX PI Lynch KJ, Burgard EC, Metzger RE, Niforatos W, Touma EB;
XX PI Van Biesen T;
XX
XX DR WPI: 2001-388837/41.
XX DR P-PSDB; AAB84382.
XX
XX Isolated polynucleotides, used to produce P2X2 receptor polypeptides and
XX identify potentially therapeutic compounds, encode a human P2X2
XX receptor polypeptide -
XX
XX Example 4; Fig 11; 40pp; English.
XX
XX The specification describes nucleic acids encoding a functional human
XX purinoreceptor polypeptides P2X2 and P2X4. P2X polypeptides and
XX polynucleotides are used to identify modulators, which may be used to
XX treat and prevent pain, diseases of the neuroendocrine system, and
XX auditory and vestibular disorders. P2X and P2X polynucleotides are a
XX source of probes and primers, which may be used to identify homologous
XX sequences, for gene localisation studies, and for gene therapy purposes.
XX The polynucleotides may also be used to produce the polypeptide
XX recombinantly. The P2X polypeptides are used to arise antibodies, and
XX to identify inhibitors. The present sequence encodes human P2X4.
XX
XX Sequence 1206 BP; 285 A; 335 C; 320 G; 266 T; 0 other;
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Query Match 12.7%; Score 235.4; DB 22; Length 1206;
Best Local Similarity 54.3%; Pred. No. 3.5e-54;
Matches 573; Conservative 5; Mismatches 441; Indels 36; Gaps 4;
Qy 55 TTTTCCAGTATGAGACGACAAACAGATCCTCGGATCCGACGATGATATGACACCATTA 114
Db 55 TTTTCCAGTATGAGACGACGACGATCCTCGGATCCTCGGATCCTCGGATCCTCGGATC 114
Qy 115 AGTGTCTTCCAGCTGATCATCTTTTCTCTAGC---TTTGTCTTGTCTGTGTGTGTGACA 171
Db 115 ACCGCGGCTGCACTGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 174
Qy 172 AGCTTACACCGGAAAGAGCCCTGTCACTTCTGTGACACCAAGGTAAGGGATAG 231
Db 175 AGGGCTACAGGAAACTGATCTCGTGGTCACTCCGTTAGCAGCAAGGTCAGGCGGTGG 234
Qy 232 CAGAGGTGAAGAGGAGATCGYGGGAATGAGTGAAGAGTGTGGTGCACAGTGTCTTTG 291
Db 235 CTGTGACCAACACTCTTAACATGGATTCGCGATCTGGGATGTGGCGGATTAATGTGATAC 294
Qy 292 ACACCGCAGACTACACCTTCCCTTTTCAGGGGAATCTTTTTCGTGTGATGACAACTTTC 351
Db 295 CAG-----CTCAGGAGGAAACTCCCTCTTCGTCATGACCAACGTGA 336
Qy 352 TCAAAACAGAGGCCAGAGACGAGCGGTGTGTCGCGAGTATCCACCCCGACGAGAGCTCT 411
Db 337 TCTCATCATGACCAACAGACAGAGCGGCTGTGCTGCCCGAGATTCAGATGCGACCACTGT 396
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Db      777 TCTGCCCATATTCCTCTGGCAACATCGTGGGGACGGGACATAGCTCCAGAGA 836
Qy      760 KGGCAATTCAGGGGGAATAATGGGCAATTCAGTCTAGTGGGACTCAACCTAGAACGTT 819
Db      837 TGGCAGTTGAGGGAGGCATCATGGGTATCCAGATCAAGTGGGACTGCAACCTGGATAG 896
Qy      820 GGTTCATCACTGCTCCCAATACAGTTTCCTCGCTTGAAGCAAGACCAACCAAG 879
Db      897 CGGCTCCCTTGGCTGGCCAGATATTCCTTCGGGCGCTTGGACACCGGAGCTGGAAC 956
Qy      880 TGTCTTTACCTGGCTACAACTTCAGATACGCAAGTACTACAGAG--AAACAATG 936
Db      957 ACAATGTCTCTCTGGCTACAACTTCAGTGTTCGCAAGTACTACAGGACCTGGCGCA 1016
Qy      937 TTGAGAAAGGACTCTGTAAGTCTTCGGGATTCCTTTGATACCTCGTTTGGCA 996
Db      1017 AAGACAGCGACACTACCAAGGCGTACGGCATCCGCTTGGATCATCGTGTGGAA 1076
Qy      997 CGGAGGAAATTTGACATATCCAGCTGGTGTGTATACGCGCTCAACCTCTCTACT 1056
Db      1077 AGCTGGGAGTTTGACATATCCCTACATGATCAACGTGGCTGTGGCTGTC 1136
Qy      1057 TCGGCTGGGCTGTGTTCATCGACTTCCTCATC 1091
Db      1137 TCGGGTGGGACGGTCTCTGTGTGACGTATGTC 1171

RESULT 10
AAD04979
ID AAD04979 standard; DNA; 1207 BP.
AC AAD04979;
XX
DT 17-JUL-2001 (first entry)
DE
XX
XX Human purinergic receptor P2X4 receptor DNA.
XX Human; purinergic receptor; P2X4; antidepressant; vulnerary; hypotensive;
KW anticonvulsant; antiinflammatory; therapy; nervous system disorder;
KW epilepsy; pain; depression; neurodegenerative disorder; cystic fibrosis;
KW irritable bowel disorder; reproductive system disorder; hypertension;
KW peripheral vascular disease; immune system disorder; chronic bronchitis;
KW premature ejaculation; asthma; neuromuscular disease; ds.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 21..1186
XX FT /*tag= a
XX FT /product= "Human P2X4 receptor."
XX FT misc_feature 263
XX FT /*tag= b
XX FT /*note= "Represented in the specification as P"
XX
XX US6214581-B1.
XX
XX 10-APR-2001.
XX
XX 13-NOV-1998; 98US-0191136.
XX
XX 16-JAN-1998; 98US-0071298.
XX 16-JAN-1998; 98US-0071669.
XX 16-JAN-1998; 98US-0008185.
XX 16-JAN-1998; 98US-0008526.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Lynch KJ, Burgard EC, Van Biesen T;
XX WPI; 2001-315459/33.
XX
XX Novel isolated polynucleotide encoding human purinergic P2X3 receptor

```

```

PT polypeptide useful for identifying potentially therapeutic compounds
PT that modulate or otherwise interact with P2X containing receptors -
XX
XX Example 11; Fig 10; 53pp; English.
XX
XX The present sequence is human P2X4 receptor DNA containing its open
XX reading frame with EcoRI restriction used for subcloning. P2X
XX receptors are ligand-gated ion channels while P2X receptors operate
XX generally through a G-protein coupled system. P2X purinoreceptor drugs
XX are potential therapeutic agents in several disorders including central
XX nervous system or peripheral nervous system conditions, e.g., epilepsy,
XX pain, depression, neurodegenerative disorders, disorders of the skeletal
XX muscle such as neuromuscular diseases, disorders of the reproductive
XX system, asthma, peripheral vascular disease, hypertension, immune system
XX disorders, irritable bowel disorder, premature ejaculation, cystic
XX fibrosis and chronic bronchitis. P2X purinoreceptors mediate the activity
XX of extracellular nucleotide triphosphates to regulate chloride secretion
XX in human airway epithelia.
XX
XX Sequence 1207 BP; 285 A; 335 C; 320 G; 266 T; 1 other;

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Query Match 12.6%; Score 233.8; DB 22; Length 1207;
Best Local Similarity 54.9%; Pred. No. 9.7e-54;
Matches 581; Conservative 4; Mismatches 432; Indels 41; Gaps 5;
Qy 55 TTTTCCAGTATGAGACGACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTA 114
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 115 AGTGGTTCTTCCAGGTGATCATCTTTTCTACG---TTTGGCTTTGCTGCTGAGTGACA 171
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 115 ACCGCGCGGTGCAACTGCTCATCTCTGGCTACGTCATCGGTGGTGTGTTGCTGGGAAA 174
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 172 AGCTGTACAGCGGAAGAGAGCTGTATCATGTTCTGTGCACACCAAGTGAAGGAGTAG 231
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 175 AGGGCTACCAAGAACTGACTCCGTGGTCAAGCTCCGTACGACCAAGGTCAAGGGGTGG 234
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 232 CAGAGGTGAAGAGGAGATCGTGGAGATGAGTGAAGAGTGGTGCACAGTGTCTTTG 291
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 235 CTGTGACCAAC-----ACTTCTAACTTGGATTTCGGATCTGGG 274
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 292 ACACCGCAGACTACACTTCC---CTTTGAGGGGAACTCTTTCTGCTGATGACAAACT 348
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 275 ATGTGGGGATATGTGATACAGCTCAGGAGGAAAACTCCCTCTGCTCATGACCAACG 334
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 349 TTCTCAAAACAGAGCGCCAGAGCAGCGGTGTGTCCTCCGATATCCACCGCAGGACGC 408
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 335 TGATCTCTACCATGAAACCCAGACAGAGGCTGTGCCCGAGATTCAGATCGGACACTG 394
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 409 TCTGTTCTCTGACCGAGGTTGTAAAAAGGATGAGTGGACCCCGCAGAGCAAGGAACTC 468
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 395 TGTGTAAATCAGATGCCAGCTGTACTGCGGCTCTCGCGSCACCCACAGCAAGGATCT 454
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 469 AGACCGGAAGTGTGTAGTATGAGGGACACAGAGACCTGTGAGTCTCTCCCTGGT 528
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 455 CAACAGCGCAGGTGCTGAGTCTTCAACGGGTCCGTCAAGACGTGTGAGGTGCGGCTGT 514
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 529 GCCCATCGGAGCGTGGAGAGGCGCCCGGCTGTCTCTTTGAACAGTGCAGGAAACT 588
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 515 GCCCGTGGAGGATGACACACGTGCCCAACCTGCTTTTAAAGGCTCGCAAAACT 574
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 589 TCACTGTGCTCATCAAGAACAAATATCGACTTCCCGCCACCAACTACACCAAGGAAACA 648
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 575 TCACTCTTTTGGTTAAGAACAACTGCTGTATCCCAATTTAATTTACGCAAGGAAATA 634
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 649 TCCTGCCAGGTTAAACATCACT-----TGTACCTTCCACAGACTCAGAAATC 696
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 635 TCCTTCCCAACATCACTCACTTACTTACCTCAAGTGTGCTATTTATGATGCTAAAAAGATC 694
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 697 CACAGTGTCCCATTTTCCGACTTAGGAGACATCTTCCGAGAAACAGGCGATATATTTTCAG 756
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 695 CCTTCTGCCCATATTCCTCTGTGGCAAAATGATGGAGAACGACGAGGACGCTTCAGG 754
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 757 ATGKGAATTCAGGCGGAAATATGGCAATTCAGATCTACTGGACTGCAACTAGACC 816
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 755 ACATGCGCTGGAGGAGGATCATGGGCTCCAGTCACTGGGACTGCACTGGACA 814
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 817 GTTGGTTCATCACTGCGCTCCCAATACAGTTTCCTGCGCTTGACGACAGACCA 876
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 877 ACATGCGCTGGAGGAGGATCATGGGCTCCAGTCACTGGGACTGCACTGGACA 874
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 875 AGCACAACATCTCTCGCTGCTACAAATTCAGTTTCCCAAGTACTACAGAGACTGGCTG 934
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 937 ---TTGAGAAACGGACTCTGATAAAAGTCTGGGATCGTTTGACATCTGCTGTTTG 993
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 935 GCACAGAGAGCGGACGCTCATCGGCTTATGGCATCGCTTCGACATCATTTGTTTG 994
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 994 GCACCGGAGAGAAATTTGACATTTATCCAGCTGGTGTGTGTATCATCGCTCAACCTCTCT 1053
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 995 GGAAGCAGGAGAAATTTGACATCATCCACATATGATCATCATCGCTCTGGCTGGCAC 1054
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 1054 ACTTCGCTGCGGCTGCTGTTTCATCGACTTCCTCATC 1091
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 1055 TECTAGGATCGGACCGCTGCTGTGTGTGACATCATAGTC 1092
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
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RESULT 11

```
AAV09308
ID AAV09308 standard; DNA; 1807 BP.
AC AAV09308;
DT 18-MAY-1998 (first entry)
XX Human brain P2X-2 receptor encoding cDNA.
DE Brain; P2X receptor; treatment; trauma; spinal cord; infection;
KW human; inflammation; mood disorder; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FT 14..1228
FT CDS /tag= a
FT /product= "Human brain P2X-2 receptor"
FT insertion_seq 148..196
FT /tag= b
FT /note= "48 base pair insertion to P2X-1 receptor
FT generates P2X-2 receptor"
```

```
W09741222-A1.
XX 06-NOV-1997.
XX 30-APR-1996; 96WO-GB01034.
XX 30-APR-1996; 96WO-GB01034.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX Carpenter DJ, Livingstone CD, McHALE NT, Tomlinson WJ;
XX Yi L;
XX WPI; 1997-549726/50.
XX P-PSDB; AAW47067.
XX DNA encoding human brain P2x receptors - used to develop products
XX for treating, e.g. brain or spinal cord traumas, infection,
XX inflammation and mood disorders
XX Claim 6; Fig 2; 31pp; English.
XX This cDNA encodes a human brain P2X-2 receptor polypeptide. The P2X
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CC receptor splice variants (P2X-1, P2X-2 and P2X-3 isoforms) can be
CC recombinantly expressed by a host cell genetically engineered with a
CC vector containing the encoding nucleic acids. The receptors can be used
CC to screen for their antagonists. The products can be used to identify
CC agents which modulate the activity of the receptors for use in clinical
CC conditions such as brain stroke, brain or spinal cord traumas, infection
CC and inflammation, cognitive disorders, epilepsy, affective and mood
CC disorders in general, including depression, various movement disorders
CC including Parkinson's disease, Huntingtons Chorea and schizophrenia, as
CC well as those conditions that are associated with the development of
CC chronic or acute forms of pain, or cardiac anoxia. The products can also
CC be used for detection, production of antibodies and production of
CC transgenic animals as models for mutation and structure/activity
CC relationship evaluations as well as in drug screening.
XX Sequence 1807 BP; 415 A; 507 C; 493 G; 392 T; 0 other;
QY Query Match 12.3%; Score 227.2; DB 18; Length 1807;
Db Best Local Similarity 57.1%; Pred. No. 7.7e-52;
Matches 453; Conservative 4; Mismatches 322; Indels 15; Gaps 2;
QY 313 CTTTGAGGGGAACCTTTCTTCGTGATGACAAACTTTCTCAAAACAGAGAGCCAGAGC 372
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 339 CTCAGGAGGAAACTCCCTCTTCGTATGACCAACGCTGATCTCACCATGACACACAC 398
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 373 AGCGGTTGTCCCGATATCCACCAGGACGCTGTGTTCTCTGACGAGGTTGTA 432
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 399 AGGCGCTGTCCCGAGATTCAGATCGACACCTGTGTGTAATCATGATGCCAGTGTA 458
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 433 AARAGGATGGATGACCCCGAGAGCAAGAAATTCAGACCGGAGGTGTGTAGTATG 492
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 459 CTGCGCGCTCTGCCCGACCCACAGCAAGGAGTCTCAACAGGAGGTGCGTACTTCA 518
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 493 AAGGGAACAGAGACCTGTGAAGTCTCTGCTGTGTCGCCCATCGAGGAGTGAAGAGG 552
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 519 ACGGGCTGTCAAGACGCTGTGAGGTGGCGCTGTGTCGCCGTGAGGATGACACACAG 578
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 553 CCCCCCGGCTCTCTCTTTGAACAGTCCGAAACCTTCACTGTCTCATCAAGAACATA 612
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 579 TGCCACAACCTGCTTTTAAAGGTCGCAAAACCTTCACTCTTTTGGTTAAGAACACA 638
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 613 TCGACTTCCCGGCGCACACTACACAGAGAAACATCTCGCCAGGTTTAAACATCACT- 671
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 639 TCTGGTATCCCAATTTAATTCAGCAAGAGGAAATATCTTCCCAACATCACTACTT 698
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 672 -----TGTACCTTCCACAAGACTCAGAAATCCACAGTCCCATTTTCGGACTAG 720
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 699 ACCTCAGTCTGTGATTTATGATGCTTAAACAGATCCCTTTCGCCCATATTCGGCTTG 758
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 721 GAGACATCTCCGAGAAACAGCGGATTAATTTTCAGATGCGCAATTCAGGGGGGATAA 780
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 759 GCAAAATAGTGGAGAACGCGGACACAGTTTCCAGGACATGCGCGTGGAGGGGATCA 818
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 781 TGGGCAATGAGATCTACTGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCCTCCA 840
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 819 TGGGCAATGAGATCTACTGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCCTCCA 878
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 841 AATACAGTTTCCCTGCGCTTGCAGCAAGACCAACAGTGTCTTGTACCTGGGTACA 900
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 879 GGTACTCTTCGCGGCTTCGATACACGAGGACCTTTGACGACCAACATATCTCTGGCTACA 938
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 901 ACTTCAGATACGCCAAGTACTACAGGAAACAAATG---TTGAGAAACGGGACTGTGATAA 957
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 939 ATTTCAGGTTTGCAGGACTACAGAGACCTGCTGGCAACGAGCGAGCGGACGTCATCA 998
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 958 AAGTCTTCGGGATCCGTTTTCAGATCTCTGTTTGGGACCGGAGGAAATTTGACATTA 1017
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 999 AGGCTATGCGCATCGCTTCGACATCATTTGTGTTGGGAGGCGAGGAAATTTGACATCA 1058
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 1018 TCCAGCTGTTGTGATACGCTCAACCTCTCTCTACTTCCGTTCCGCTGCTGCTTCA 1077
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
QY 1059 TCCCACTATGATCAACATCGGCTCTGCGCTGCGACTGCTAGGATGCGGACCGCTCT 1118
Db | :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
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Qy 1078 TCGACTTCTCTCATC 1091
 Db 1119 GTGACATCATGTC 1132

RESULT 12

ID ABK84338 standard; cDNA; 2633 BP.

XX ABK84338;

XX 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #909.

XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.

XX Homo sapiens.

XX W0200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US30821.

XX 03-OCT-2000; 2000US-237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

XX Detecting granulocyte activation by detecting differential expression
 of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity -

XX Claim 1; SEQ ID No 909; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting the
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC an allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal

CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection, and M5 is
 CC parasitic infection, protozoal infection, fungal infection, and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 2633 BP; 582 A; 804 C; 701 G; 546 T; 0 other;

Query Match 11.0%; Score 203.8; DB 24; Length 2633;

Best Local Similarity 54.8%; Pred. No. 2.5e-45;

Matches 447; Conservative 5; Mismatches 342; Indels 21; Gaps 2;

Qy 285 GTCTTTGACACCGCAGACATACACCTTCCTTTCAGGGGAACTCTTCTCGTGATGACA 344

Db 446 GTCTGGGATGGCTGACTAAGTCTTCCAGCCAGGGGGACAACTCTCTGGTGTATG 505

Qy 345 TACTTTCTCAAAACAGAGGCCAAGAGCGGTTGTGCCGAGTATCCACACCGGAGG 404

Db 506 ACCAATTTCATCGTGACCCCGGAAGCAGACTCAAGGCTACTGGCAGAGCACCACGAAGG 565

Qy 405 AGGCTCTGTTCTCTGACCGAGGTGTAAAGAGGATGGATGACCCGACAGCAAGGA 464

Db 566 GGCATATGCAAGAGACAGAGTGGCTGTACCCCTGGGAAGCCAGAGGAGCCCAAGG 625

Qy 465 ATTCAGACCGGAAAGGTGTAGTATYANGAAGGGAACCAAGAACCTGTGAAGTCTCTGCC 524

Db 626 ATCCGACGGGCAAGTGTGTGGCTTCAACGACACTGTGAAGAGCTGTGAGATCTTTGGC 685

Qy 525 TGGTGGCCCTTCGAGGAGTGGAGAGAGCCGCCCGGCTGCTCTTGAACAGTGGCGAA 584

Db 686 TGGTGGCCCTTCGAGGAGTGGAGAGAGTCCCGGCGCTGCTCTTGAACAGAGCCGAG 745

Qy 585 TACTTCACTGTCTCATCAAGAACATATGACTTCCCGGCAACACTACACACAGAGA 644

Db 746 TACTTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCGC 805

Qy 645 TACTTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 692

Db 806 TACTTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 865

Qy 693 TACTTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 752

Db 866 TACTTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 925

Qy 753 TCAAGTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 812

Db 926 TCAAGTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 985

Qy 813 TCAAGTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 872

Db 986 TCAAGTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 1045

Qy 873 TCAAGTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 932

Db 1046 TCAAGTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 1096

Qy 933 TCAAGTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 992

Db 1097 TCAAGTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 1156

Qy 993 TCAAGTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 1052

Db 1157 TCAAGTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 1216

Qy 1053 TCAAGTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 1087

Db 1217 TCAAGTCACTGTCTCATCAAGAACATAGCTTCCAGGCTTCAAGGTCAACAGGCTCAAG 1251

RESULT 13	
ABL70017	
ID	ABL70017 standard; DNA; 2633 BP.
XX	
AC	ABL70017;
XX	
DT	15-MAY-2002 (first entry)
XX	
DE	Pancreas cancer related gene sequence SEQ ID NO:8354.
XX	
DE	
XX	
KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytostatic; gene therapy; anti-neoplastic; Wilms' tumour; adenocarcinoma;
XX	gene; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200194629-A2.
XX	
PD	13-DEC-2001.
XX	
PF	30-MAY-2001; 2001WO-US10838.
XX	
PR	05-JUN-2000; 2000US-209473P.
PR	05-JUN-2000; 2000US-209531P.
PR	18-SEP-2000; 2000US-233133P.
PR	18-SEP-2000; 2000US-233617P.
PR	20-SEP-2000; 2000US-234009P.
PR	20-SEP-2000; 2000US-234034P.
PR	20-SEP-2000; 2000US-234052P.
PR	22-SEP-2000; 2000US-234509P.
PR	22-SEP-2000; 2000US-234567P.
PR	25-SEP-2000; 2000US-234923P.
PR	25-SEP-2000; 2000US-234924P.
PR	25-SEP-2000; 2000US-235077P.
PR	25-SEP-2000; 2000US-235082P.
PR	25-SEP-2000; 2000US-235134P.
PR	25-SEP-2000; 2000US-235280P.
PR	26-SEP-2000; 2000US-235637P.
PR	26-SEP-2000; 2000US-235638P.
PR	27-SEP-2000; 2000US-235711P.
PR	27-SEP-2000; 2000US-235720P.
PR	27-SEP-2000; 2000US-235840P.
PR	27-SEP-2000; 2000US-235863P.
PR	28-SEP-2000; 2000US-236028P.
PR	28-SEP-2000; 2000US-236032P.
PR	28-SEP-2000; 2000US-236033P.
PR	28-SEP-2000; 2000US-236034P.
PR	28-SEP-2000; 2000US-236109P.
PR	28-SEP-2000; 2000US-236111P.
PR	29-SEP-2000; 2000US-236844P.
PR	29-SEP-2000; 2000US-236869P.
PR	02-OCT-2000; 2000US-237172P.
PR	02-OCT-2000; 2000US-237173P.
PR	02-OCT-2000; 2000US-237278P.
PR	02-OCT-2000; 2000US-237294P.
PR	02-OCT-2000; 2000US-237295P.
PR	02-OCT-2000; 2000US-237316P.
PR	03-OCT-2000; 2000US-237425P.
PR	03-OCT-2000; 2000US-237598P.
PR	03-OCT-2000; 2000US-237604P.
PR	03-OCT-2000; 2000US-237605P.
PR	03-OCT-2000; 2000US-237608P.
PR	01-NOV-2000; 2000US-244867P.
PR	01-NOV-2000; 2000US-245084P.
XX	
PA	(AVAL-) AVALON PHARM.
XX	
PI	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI	Soppet DR, Weaver Z;
XX	
DR	WPI; 2002-188264/24.

Db 1046 A-----AFCCTCCCGAGGCTCAACTTCAGGTTGCCAGGACATTTGTGGAGAC 1096
 QY 933 AATGTTGAGAAACGAGCTCTGATAAAGTCTTCGGGATCCGTTTGAACATCCTGGTTTTT 992
 Db 1097 GGGACCAACTACCGTCACTCTTCAAGGTGTTTGGGATTCGCTTTCACATCCTGGTGGAC 1156
 QY 993 GGCACCGGAGAAATTTGACATTTATGACATGTTTCCAGTCTGTGTGATCATCGCAACCTCTCC 1052
 Db 1157 GGCAGGCGGGAAGTTGACATCAATCCCTACATGACACCAATCGGCTCTGGAATTGGC 1216
 QY 1053 TACTTCGCTCGCCCTCTGTGTCATCGACTTCCT 1087
 Db 1217 ATCTTTGGGGTGGCCACAGTCTCTGTGAACCTGCT 1251

RESULT 14

ID AAT33855 standard; cDNA; 2643 BP.

AC AAT33855;

DT 23-NOV-1996 (first entry)

XX Human urinary bladder P2x receptor cDNA.

XX ATP P2x receptor; purinoceptor; ligand-gated ion channel; agonist;
 KW antagonist; epilepsy; cognition; emesis; pain; asthma;
 KW peripheral vascular disease; hypertension; irritable bowel syndrome;
 KW premature ejaculation; cystitis; therapy; ss.

XX Homo sapiens.

PH Key Location/Qualifiers
 FT CDS 174..1373
 FT /*tag= a

PN W09533048-A2.

PD 07-DEC-1995.

XX 24-MAY-1995; 95WO-EP01968.

PR 09-FEB-1995; 95GB-0002480.

PR 27-MAY-1994; 94GB-0010664.

XX (GLAX) GLAXO GROUP LTD.

PI Buell GN, Valera S;

XX WPI; 1996-030561/03.

DR P-PSDB; AAW04218.

XX DNA encoding ATP P2x receptors of the purinoceptor family - for
 PT screening cpds. useful in treating epilepsy, cognition, emesis,
 PT pain, asthma, peripheral vascular disease, hypertension, etc.

XX Claim 1; Fig 4; 82pp; English.

XX A cDNA clone (AAT33855) codes for the human urinary bladder P2x
 CC receptor (AAW04218), a ligand-gated ion channel that opens upon
 CC binding of extracellular ATP. It was isolated from a bladder
 CC cDNA library using a rat smooth muscle P2x receptor probe.
 CC Rat vas deferens, superior cervical ganglion and dorsal root
 CC ganglion P2x receptor cDNAs (AAT33852-54) have also been isolated.
 CC These cDNAs can be used to produce recombinant P2x receptors in
 CC host, esp. mammalian, cells for use in screening (ant)agonist
 CC cpds.

XX Sequence 2643 BP; 607 A; 794 C; 701 G; 541 T; 0 other;

XX Query Match

XX Best Local Similarity 54.8%; Pred. No. 2.6e-45; Length 2643;

XX Matches 447; Conservative 5; Mismatches 342; Indels 21; Gaps 2;

QY 285 GTCTTTGACACCGCAGACTACACCTTCCCTTCAGGGGAACTCTTCTTCGTGATGACA 344
 Db 423 TCTTGGGATGSGCTAGCTAGCTTCCAGCCAGGGGCAAACTCCTTCGTGGTCAATG 482
 QY 345 AACTTTCTCAAAACAGAGGCAAGAGCAGCGGTGTGTCCCGAGATCCCAACCCGAGG 404
 Db 493 ACCAATTCATCGTGCCCGGAGCAGACTCAAGSGTACTGGCAGAGCACCAGAGGG 542
 QY 405 AGCTCTGTTCCTCTGACCGAGGTTGTAAAGAGGATGATGAGCCCGCAGAGCAAGA 464
 Db 543 GGCATATGCAAGGAAGACAGTGGCTGTACCCCTGGGAGGCCAAGAGGAAGGCCAAGGC 602
 QY 465 ATTCAGACCGGAGGTGTGTAGTATGAGGGAACACAGAGACTGTGAGTCTCTGCC 524
 Db 603 ATCCGCACGGGCAAGTGTGTGGCTTCAACGACACTGTGAAGAGCTGTGAGATCTTTGGC 662
 QY 525 TGGTCCCGCATCGAGGAGTGAAGAGGCCCCCGGCTGTCTCTTGAACAGTGCAGAA 584
 Db 653 TGGTCCCGCTGGAGTGGATGAGACATCCCGGCCCTGCCCTTCCGAGAGGCCGAG 722
 QY 585 AACTTCACTGTCTATCAGAGCAATATGCAATTTCCCGGCGCACAGTACACACAGAGA 644
 Db 723 AACTTCACTCTTTTATCAAGAACAGCATCAGTGTTCACGCTTCAAGGTCAACAGGCG 782
 QY 645 AACATCTCTCCAGGTTTAAA-----CATCACTTGTAACCTTCCACAGACTCAG 692
 Db 793 AACTGTTGAGAGGTGAATGCTGCCACATGAAGACCTGCCCTTTCACAGACCCCTG 842
 QY 693 AATCCAGTGTCCCATTTTCCGACTAGGAGACATCTCCGAGAAACAGGCGATAATTT 752
 Db 843 CACCCCTGTGCGCCAGTCTTCCAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
 QY 753 TCAGATGKGCATTCAGGCGGATATGAGGATTCAGATCTACTCGGACTGCACACCTA 812
 Db 903 AGCACCCCTGGCTGAGAAGGGTGGAGTGGTGGCATCACCATCGACTGCTGACCTG 962
 QY 813 GACCGTTGGTTCCATCACTGCTCCCAATACAGTTTCCRTCCGCTTGACAGCAAGAC 872
 Db 963 GACTGGCAGCTGACGGCCTGACAGCCCATCTATGACTTCCATGGCTGTACGAGAGAA 1022
 QY 873 ACCAAGCTGCTTGTACCTGGCTGACACTTCACTGATGAGCCCAAGTACTACAGGAAAC 932
 Db 1023 A-----ATCTCTCCCGAGGCTTCAACTTCAGSTTTTCCAGGCACTTTTGGGAAAC 1073
 QY 933 AATGTTGAGAACGAGTCTGTATAAAGTCTTCGGGATCCGTTTGGATCGATCGCTGTTT 992
 Db 1074 GGGACCAACTACCGTCACCTCTTCAAGGTGTTTGGGATTCGCTTTGACATCCTGGTGAC 1133
 QY 993 GGCACCGGAGGAAATTTGACATTTACAGTGGTGTGTATCATCGGCTCAACCTCTCC 1052
 Db 1134 GGCAGCGCGGGAAGTTTGACATCATCCCTACATGACCAACCATCGGCTCTGGAATTGGC 1193
 QY 1053 TACTTGGCTGCGCCCTCTGTGTCTATCGACTTCCT 1087
 Db 1194 ATCTTTGGGGTGGCCACAGTCTCTCTGTGACCTGCT 1228

RESULT 15

ID AAV89619 standard; cDNA; 294 BP.

AC AAV89619;

XX 15-FEB-1999 (first entry)

DE EST clone C0390.

XX Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
 KW tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
 KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
 XX gene therapy; ss.

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OS Homo sapiens.
XX
PN WO9845436-A2.
XX
PD 15-OCT-1998.
XX
PF 10-APR-1998; 98WC-US06955.
XX
PR 10-APR-1997; 97US-0838821.
XX
PA (GENY ) GENETICS INST INC.
XX
PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI Racie LA, Spaulding V, Treacy M;
XX
DR WPI; 1999-070077/06.
XX
PT New polynucleotides encoding human secreted proteins - derived from
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT ovary, pituitary, retina and colon cDNA libraries.
XX
PS Claim 1; Page 276; 618pp; English.
XX
CC The present sequence represents a human expressed sequence tag (EST).
CC The polynucleotide, which is a secreted EST, and the encoded protein
CC are predicted to have useful biological activities which would make
CC them suitable for treating, preventing or ameliorating medical
CC conditions in humans and animals, although no supporting data is
CC given. Suggested activities include nutritional activity, immune
CC stimulating or suppressing activity, haematopoiesis regulating
CC activity, tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
CC activity, receptor/ligand activity, anti-inflammatory activity,
CC cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity. The polynucleotide may also be useful for gene therapy.
XX
SQ Sequence 294 BP; 81 A; 72 C; 68 G; 73 T; 0 other;

Query Match 10.6%; Score 196.4; DB 20; Length 294;
Best Local Similarity 98.5%; Pred. No. 9.1e-44;
Matches 197; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 576 AGTCCGAAACCTCTGCTCATCAAGAACAAATATCGACTTCCCGGCCCACTAC 635
Db |||||||
30 AGTCCGAAACCTCTGCTCATCAAGAACAAATATCGACTTCCCGGCCCACTAC 89
QY 636 ACCACGAGAAACATCTGCTGAGTTTAAACATCTGTACCTTCCACAGACTCAGAT 695
Db |||||||
90 ACCACGAGAAACATCTGCTGAGTTTAAACATCTGTACCTTCCACAGACTCAGAT 149
QY 696 CCACAGTGTCCATTTTCCGACTAGGACATCTTCGGAGAAACAGGCGATATTTC 755
Db |||||||
150 CCACAGTGTCCATTTTCCGACTAGGACATCTTCGGAGAAACAGGCGATATTTC 209
QY 756 GATGCGCAATTCAGGCGG 775
Db |||||||
210 GATGCGCAATTCAGGCGG 229
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Search completed: July 18, 2003, 20:53:32
Job time : 455 secs

1	AAACGCGAGGAGGAGCTGTGCACCATCCGGCCCTGTCAGCTGCAGTGAATGTTTCC	60
1	AAAACGCGAGGAGGAGCTGTACCATCGCGCCCTGTCAGCTGCAGTGAATGTTTCC	60
61	AGTATGAGACGAAACAAGTCACTCGGATCCAGACATGAATATGCGACCAATTAAGTGGT	120
61	AGTATGAGACGAAACAAGTCACTCGGATCCAGACATGAATATGCGACCAATTAAGTGGT	120
121	TCCTCCACGTGATCATCTTTCTACGTTTCTTCTGCTGCTGAGTGAACAAGCTGTACC	180
121	TCCTCCACGTGATCATCTTTCTACGTTTCTTCTGCTGCTGAGTGAACAAGCTGTACC	180
181	AGCGGAAAGAGCCGTGCATAGTCTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGA	240
181	AGCGGAAAGAGCCGTGCATAGTCTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGA	240
241	AAGAGGAGATCGYGAGAAATGGAGTGAAGAATTTGGTGCACAGTGTCTTTGACACCGCAG	300
241	AAGAGGAGATCGTGGAAATGGAGTGAAGAATTTGGTGCACAGTGTCTTTGACACCGCAG	300
301	ACTACACCTTCCTTTGAGGGGAATCTTTCTCGTGATGACAAACTTTCACAAAACAG	360
301	ACTACACCTTCCTTTGAGGGGAATCTTTCTCGTGATGACAAACTTTCACAAAACAG	360

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QY 361 AAGGCCAAGACGACGGTGTGTCGCGAGTATCCCAACCCGCGAGGAGCTGCTGTCCTCTG 420
Db 361 AAGGCCAAGACGACGGTGTGTCGCGAGTATCCCAACCCGCGAGGAGCTGCTGTCCTCTG 420
QY 421 ACCGAGGTGTAAAGAGGATGATGGACCCGCGAGACAAAGAAATTCAGACCGGAAAGGT 480
Db 421 ACCGAGGTGTAAAGAGGATGATGGACCCGCGAGACAAAGAAATTCAGACCGGAAAGGT 480
QY 481 GTGTAGTATYATGAAGGAAACAGAGACCTGTGAAGTCTCTGCTGGTGCCTCATCGAGG 540
Db 481 GTGTAGTATCATGAAGGAAACAGAGACCTGTGAAGTCTCTGCTGGTGCCTCATCGAGG 540
QY 541 CAGTGAAGAGCCGCCGCGCTGCTCTGTAACAGTGCAGGAAACTTCATGTGTCTCA 600
Db 541 CAGTGAAGAGCCGCCGCGCTGCTCTGTAACAGTGCAGGAAACTTCATGTGTCTCA 600
QY 601 TCAAGAAACAATATGACTTCCCGGCGCACAACTACACAGAGAAACATCTTCGCAGGTT 660
Db 601 TCAAGAAACAATATGACTTCCCGGCGCACAACTACACAGAGAAACATCTTCGCAGGTT 660
QY 661 TAAACATCACTGTACCTTCCACAGACTCAGAACTCAGAGTGTCCATTTTCCGACTAG 720
Db 661 TAAACATCACTGTACCTTCCACAGACTCAGAACTCAGAGTGTCCATTTTCCGACTAG 720
QY 721 GAGACATCTCCGAGAAACAGGCGATAATTTTCAGATGKGGCAATTCAGGCGGGAATAA 780
Db 721 GAGACATCTCCGAGAAACAGGCGATAATTTTCAGATGKGGCAATTCAGGCGGGAATAA 780
QY 781 TGGGCAATGAGATCACTGAGGACTGCAACTAGACCGTGGTTCCTACACTGCCRTCCCA 840
Db 781 TGGGCAATGAGATCACTGAGGACTGCAACTAGACCGTGGTTCCTACACTGCCRTCCCA 840
QY 841 AATACAGTTCCTCGCTTGAGCAGACAGACACACAGCTGCTGTACCTGCTGCTGCTACA 900
Db 841 AATACAGTTCCTCGCTTGAGCAGACAGACACACAGCTGCTGTACCTGCTGCTGCTACA 900
QY 901 ACTTCAGATGAGCCCAAGTACTACAGGAAACAATGTGTGAGAACGAGACTGTGATAAAG 960
Db 901 ACTTCAGATGAGCCCAAGTACTACAGGAAACAATGTGTGAGAACGAGACTGTGATAAAG 960
QY 961 TCTTGGGATCGGTTTGTGATCCTGTTTGGACCGGAGGAAATTTGACATATATCC 1020
Db 961 TCTTGGGATCGGTTTGTGATCCTGTTTGGACCGGAGGAAATTTGACATATATCC 1020
QY 1021 AGCTGTTGTGTCATGCGCTCAACCTCTCTACTTCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 AGCTGTTGTGTCATGCGCTCAACCTCTCTACTTCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 ACTTCCTCATGACACTTACTCCAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1081 ACTTCCTCATGACACTTACTCCAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1141 ASGTGCTGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1141 ASGTGCTGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 TGGAGCCAAAGCCGACATTAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1201 TGGAGCCAAAGCCGACATTAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1261 TGAACCAAGAGTACTAGGAGAGTCTGCAAGATGTCAAGGCTGCAAGGCTGCAAGGCTG 1320
Db 1261 TGAACCAAGAGTACTAGGAGAGTCTGCAAGATGTCAAGGCTGCAAGGCTGCAAGGCTG 1320
QY 1321 CTGAGTACGCTTACAGATTTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTG 1380
Db 1321 CTGAGTACGCTTACAGATTTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTG 1380
QY 1381 TTCTTGGACCAACAGGAGATACAGCTGCTTAGAAGAGGAGGAGGAGGAGGAGGAGGAG 1440
Db 1381 TTCTTGGACCAACAGGAGATACAGCTGCTTAGAAGAGGAGGAGGAGGAGGAGGAGGAG 1440
QY 1441 ATAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
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Db 1441 ATAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1501 GGTGCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Db 1501 GGTGCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 TGTTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Db 1561 TGTTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
QY 1621 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 GGTAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1681 GGTAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
QY 1741 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Db 1741 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
QY 1801 AGAGTCTTACTGAGCCAGGACCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1853
Db 1801 AGAGTCTTACTGAGCCAGGACCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1853

RESULT 2
US-08-842-079-16
; Sequence 16, Application US/08842079
; Patent No. 6133434
; GENERAL INFORMATION:
; APPLICANT: BUELL, GARY N.
; APPLICANT: SUPREMAN, ANNMARIE
; TITLE OF INVENTION: A PURINERGIC RECEPTOR
; FILE REFERENCE: 1430-160
; CURRENT APPLICATION NUMBER: US/08/842,079
; CURRENT FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 3540
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-842-079-16

Query Match 69.1%; Score 1281.2; DB 3; Length 3540;
Best Local Similarity 81.4%; Pred. No. 0;
Matches 1469; Conservative 11; Mismatches 324; Indels 0; Gaps 0;

QY 11 GAGGAGAGCTGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 70
Db 106 GAGTGAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 165
QY 71 GAGCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 130
Db 166 AAGCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 225
QY 131 GATCATCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 190
Db 226 GAGCCCTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 285
QY 191 GCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 250
Db 286 GCGCCCTTATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 345
QY 251 CGYGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
Db 346 CAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 405
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QY	311	CCCTTTGCAGGGAACTCTTTCTTCGTGATGACAAACTTCTCTCAAAACAGAGGCCAAGA	370
Db	406	CCCTTTTGCAAGGGAACTCGTTCTTTTGTAAATGACAAATATCTCAAGTCAGAGGCCAAGA	465
QY	371	GCAGCGGTTGTCTCCGAGTATCCCAACCGGAGGACGCTCTGTCTTCCTGACCGAGGTG	430
Db	466	ACAGAAAGCTGTCTCTGAGTATCCACCGCGGTAAACAGTGCCATTCGACAGAGGTTG	525
QY	431	TAAAAGGATGGATGGACCGCAGACCAAGAAATTACAGACGGGAAGTGTTGATRYA	490
Db	526	TATAAAGAGTGGATGGAGCCACAAAAGTAAAGGAATCCAGACGGCAGGTGATACCTTA	585
QY	491	TGAAGGGAACACAGAGACCTGTGAAGTCTTCGCTGTGTGCCCTATCGAGGAGTGGAGA	550
Db	586	CGACACAGAAGGAAGAACCTGTCAATCTTTTCGCTGTGTCTCTGTGAGGAAGGAAGA	645
QY	551	GGCCCCCGCCGCTGCTCTCTGTGAACAGTCCGAAAACCTTCACCTGTCTCATCAAGACAA	610
Db	646	AGCCCCACGGCCTGCATCTTTGGAGAGCCCGAAAACCTTCACGCTACTCATCAGACAA	705
QY	611	TATCGACTTCCCGGCCACAACTACACACAGAGAAACATCCTGCCAGSTTTAAACATCAC	670
Db	706	TATCGACTTCCCGGCCACAACTATCTACGAGAAACATCTTACCAGGTATGAACATCTC	765
QY	671	TTGTACTCTCCACAGACTCAGAAATCCACAGTGTCCCAATTTTCCGCTACGAGACATCTT	730
Db	766	TTGTACTCTTCAAGACTTGGAAACCTCAGTGTCCCATCTCTCCGGTATAGGAGACATCTT	825
QY	731	CCGAGAAACAGCGGATAATTTTCAGATGKGCAAATCAGGCGGGAATTAATGGCATTTGA	790
Db	826	CCAGGAAATCGAGAGAACTTTACAGAGTGGCATTCTCAGGAGGAATCATGGCATTGA	885
QY	791	TAATCTACTGGGACTGCCAACTAGACCGTGTGGTTCATCATCTGCCTCCCAATACAGTTT	850
Db	886	GATCTACTGGGACTGCCAACTGGACAGCTGGTCCCATCGCTGTCAACCCAAATACAGTT	945
QY	851	CCRTCGCTTGACGACAGACCCAAACGCTGCTTTGACCTGGCTGCTCAACATTCAGATA	910
Db	946	CCGCGGCTGGAGACAGTAGTACCAATGAGTCCCTGTCTCCTGGCTACACTTCAGATA	1005
QY	911	CGCCAAGTACTACAAGGAAAAATGTTGAGAAACGGACTCTGATAAAAAGTCTTCGGGAT	970
Db	1006	CGCCAAGTACTATGAAGAAATGGCATGGAAGGCGACATGATCAAGGCTTCGCGT	1065
QY	971	CCGTTTGCATCTCGTTTGTGGCACCGGAGAAAATTTGCATATATCCAGCTGGTTGT	1030
Db	1066	CGSTTTTGACATCTCGSTTTTGTGGCATGCGAGGAAAGTTTGACATCATCCAGTTGGTGT	1125
QY	1031	GTACATCGGCTCAACCCCTCTCCTACTTGGGTGTGGCCCTGTGTATCGACTTCCCTCAT	1090
Db	1126	GTACATTTGATCCACCCGTCCTATTTTGGGTTTGGCCACCGTGTGATTTGACTTGATCAT	1185
QY	1091	CGCAASTTACTCCAGTAATCTGTGCTGCCATATTTATCCCTGGTGGAAAGTGCTGCA	1150
Db	1186	CAACAGTATGCCAGTACCTGCTGCAGGTCAAGTGTTTACCCCTTCCTGTAAAGTGTGCGA	1245
QY	1151	GCCTGTGTGGTTCACGAAATACACTACAGGAGGAAGTGGAGTCCATTTGTGGAGCCAA	1210
Db	1246	GCCTGTGCAGTGAATGTAGTACTACTACAGGAAGAAGTGTGAGCCCATCTGTGGAGCCAA	1305
QY	1211	GCCGACATAAAGTATGTCTCTTTGTGGATGAATCCACATTTAGGATGGTCAACACGA	1270
Db	1306	GCCGACCTTAAAGTATGTCTCTTTGTGGACGAGCCCAATTTGATGGTGGACACGA	1365
QY	1271	GCTACTAGGAGAAAGTCTGCAAGATGTCAAGGCGCAAGAAGTCCSAGACCTGTGATGGA	1330
Db	1366	GCTCTTGGGAAAAGTCTGCAAGATGTCAAGAGTCAAGAGTCCGAGACCCCAAGCGGA	1425
QY	1331	CTTCACAGATTTGTCCAGGCTGCCCTTGGCCCTCCATGACACACCCGCCGATTTCTTGGACA	1390
Db	1426	CTTCTTGGAACTGTCTAGGCTCTCCCTCTCTCTCTCCACCACTACCCCAATTTCTTGGACA	1485

RESIST 3

US-08-742-621-2
Sequence 2, Application US/08742621
Patent No. 5856129
GENERAL INFORMATION:
APPLICANT: HILLMAN, JENNIFER L.
APPLICANT: COLEMAN, ROGER
TITLE OF INVENTION: NOVEL HUMAN PURINOCEPTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,621
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0147 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1762 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY:
CLONE: CONSENSUS
US-08-742-621-2

Query Match 12.8%; Score 237; DB 2; Length 1762;
Best Local Similarity 54.4%; Pred. No. 7.9e-60;
Matches 574; Conservative 5; Mismatches 440; Indels 36; Gaps 4;

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QY 55 TTTTCAGTATGAGACGACAAAGTCACTCGGATCCAGAGCATGAATATGACACCAATTA 114
Db 62 TGTTCAGTATGAGACGACGCGGATCGTCTATCCGAGCGCAAGTGGGGCTCATGA 121
QY 115 AGTGGTCTTCAGAGTATGATCTTTTCTAG---TTTGGTTCCTGCTGGTGAATGACA 171
Db 122 ACCGGCGGCTCAACTCTCATCTGGCTAGTCTGCGGTGGGTGGTGGTGGGAAA 181
QY 172 AGTGTATACAGCGGAAAGAGCTGTATCATGTTCTGTGCACACCAAGGTGAAGGGATAG 231
Db 182 AGGCTACAGGAACACTGATCTCGTGTGATCGTTCAGTACACCAAGGTCAAGGGCGTGG 241
QY 232 CAGAGTGAAGAGAGATCGYGGAGATGGAGTGGTGGTGCACAGTCTCTTTG 291
Db 242 CTGTGACCAACACTTCTAACTTGGATTCCGGATCTGGGATGGCGGATTATGTGATAC 301
QY 292 ACACGCGAGATACACCTTCCCTTTCAGGGGAACCTTCTTCGTGTGATGACAAACTTC 351
Db 302 CAG-----CTCAGGAGGAAACTCCCTCTGCTCATGATGACCAACGATGA 343
QY 352 TCAAAACAGAGGCGACAGAGCGGTTGTGCCGAGTATCCACCGCGAGAGCGTCT 411
Db 344 TCCTCACCATGACACACAGAGGCGCTGTGCCGAGATTCAGATGCGACCATGTGT 403
QY 412 GTTCTCTGACGAGGTGTAAAGAGGATGATGGACCCGACAGAGCAAGGAATTCAGA 471
Db 404 GTAAATCAGATCGCAGTCTACTCGCGCTCTGCCGACCCACAGACAGCGGCTCA 463
QY 472 CGGAGGTGTGTAGTATGAGGAGGAAACAGACAGACCTGTGAGTCTGCTCTGGTCC 531
Db 464 CAGGAGGTGGCTGAGCTTTCAAGGGTCCGTCAAGACGTGTGAGGTGGCGGCTGGTCC 523
QY 532 CCATCGAGGAGTGAAGAGGCGCCCGGCTGCTCTTGAACAGTGGCGGAAACTTCA 591
Db 524 CGGTGAGGATGACACACAGCTGCCACACTGCTTTTAAAGGCTGACGAAACTTCA 583
QY 592 CTGTGCTCATCAGAACAAATATGACTTCCCGGCGCAACTACACACAGAGAAATCC 651
Db 584 CTCTTTTGTAAAGAACAACTCTGTATCCAAAATTTAATTTACGACAGAGGAATATCC 643
QY 652 TGCAGGTTTAAACATCACT-----TGTACCTTCCACAGACTCAGAAATCCAC 699
Db 644 TTCCCAATCACCACACTACTACTCAAGTCTGCTATTTATGATGCTTAAACAGATCCCT 703
QY 700 AGTGTCCCATTTCCGACTAGGACATCTCCGAGAACAGCGGATTAATTTTCAGATG 759
Db 704 TCTGCCCATATTCGCTTTGGGAAAATAGTGAGAACGAGGACACAGTTTCCAGGACA 763
QY 760 KGCATATCAGCGGGATATGGCATTTGATCTACTGGGACTGCACCTAGACCGT 819
Db 764 TGGCGGTGAGGAGGATATGGCATCCAGGTCAACTGGGACTGCAACCTGGACAG 823
QY 820 GGTTCATCACTGCGCTCCAAATACAGTTTCCRCCTTGGAGTACAGACACCAACAG 879
Db 824 CCGCTTCCCTGTCTGCCAGGTACTCTCTCCGCGGCTCGATACAGGGAGGTGAGC 883
QY 880 TGTCTTGTACCTGGCTTACACTTTCAGATAGCCCAAGTACTACAGGAAACAAATG--- 936
Db 884 ACAACGTATCTCTGGCTTACAAATTCAGGTTTGGCAAGTACTACAGAGCTGGCTGSCA 943
QY 937 TTGAGAAACGGACTCTGATAAAGTCTTCGGATCCGTTTTCAGATCCCTGGTTTGGCA 996
Db 944 ACAGAGGCGCACGCTCATCAGGCGCTATGGCATCCGCTTCGACATCATGTGTGGA 1003
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QY 997 CCGAGGAAAATTGACATATCCAGCTGGTGTGTACATCGCTCAACCCCTCTCTACT 1056
Db 1004 AGGCAGGAAAATTGACATATCCACCATATGATCAACATCGCTCTGCCTGCGACTGC 1063
QY 1057 TCGGTCTGGCGCTGTGTTCATCGACTTCCCTCANC 1091
Db 1064 TAGCATGGACGACCGTCTGTGTGACATCATAGTC 1098
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RESULT 4

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US-09-191-608-21
; Sequence 21, Application US/09191608
; Patent No. 6242216
; GENERAL INFORMATION:
; APPLICANT: Lynch, Kevin J.
; APPLICANT: Burgard, Edward C.
; APPLICANT: Metzger, Randy E.
; APPLICANT: Niforatos, Wende
; APPLICANT: Touma, Edward B.
; APPLICANT: Van Biesen, T.
; TITLE OF INVENTION: Nucleic Acids Encoding a Functional
; TITLE OF INVENTION: Human Purinoreceptor P2X2 and P2X4 And Methods Of Production
; FILE OF INVENTION: And Use Thereof
; FILE OF INVENTION: 6394.US.P1
; CURRENT APPLICATION NUMBER: US/09/191,608
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-191-608-21
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Query Match 12.7%; Score 235.4; DB 4; Length 1206;
Best Local Similarity 54.3%; Pred. No. 1.9e-59;
Matches 573; Conservative 5; Mismatches 441; Indels 36; Gaps 4;

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QY 55 TTTTTCAGTATGAGACGACAAAGTCACTCGGATCCAGAGCATGAATATGACACCAATTA 114
Db 55 TGTTCAGTATGAGACGACGCGGATCGTCTATCCGAGCGCAAGTGGGGCTCATGA 114
QY 115 AGTGGTCTTCCAGTATGATCTTTTCTAG---TTTGGTTCCTGCTGGTGAATGACA 171
Db 115 ACAGGCGCTGCAACTGCTCTCTGGCTAGTCTCGTGGTGGTGGTGGTGGGAAA 174
QY 172 AGTGTATACAGCGGAAAGAGCTGTCTATCAGTTCTGTGCACCAAGGTGAAGGGATAG 231
Db 175 AGGGTATACAGGAAACTGACTCCGTGTCAGTCCGTACGACCAAGTCAAGGGCGTGG 234
QY 232 CAGAGTGAAGAGAGATCGYGGAGATGGAGTGAAGAGTGGTGGTGCACAGTCTCTTTG 291
Db 235 CTGTGACCAACACTTCTAAACTTGGATTCCGGAATCGGGATGGCGGATTTATGTATAC 294
QY 292 ACACGCGAGATACACCTTCCCTTTCAGGGGAACCTTTCTTCGTGATGACAAACTTTC 351
Db 295 CAG-----CTCAGGAGGAAACTCCCTTTCGTATGACCAACAGTGA 336
QY 352 TCACCAACAGAGGCGACAGAGCGGTTGTGTCGAGTATCCACCCGACAGAGCGTCT 411
Db 337 TCTCACCATGAACAGACAGAGGCGCTGTGCCGAGATTCAGATGCGGACCATGTGT 396
QY 412 GTTCTCTGACCGAGTGTAAAGAGGATGGATGGTGGACCCGACAGACCAAGGAATTCAGA 471
Db 397 GTAAATCAGATCCAGCTGTACTGCGGCTTGGCGGCGCCACAGACAGGAGTCTCAA 456
QY 472 CCGGAGGTGTGTATGATGAAGGAGACCAAGAGACTGTGAGTCTCTGCTGGTCC 531
Db 457 CAGGAGGTGGCTGAGCTTTTCAAGGGTCCGTACAGAGTGTGAGGTGGCGGCTGGTCC 516
QY 532 CCATCGAGGCGAGTGAAGAGGCGCCCGGCTGCTCTTGAACAGTCCGCAAACTTCA 591
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Db 517 CGGTGGAGGATGACACACACACGCTGCCACACACCTGCTTTTAAAGGCTGCAGAAATCTCA 576
QY 592 CTGTGCTCATCAAGAACATATCGACTTCCCGGGCCACAACTACACACAGAGAAATCC 651
Db 577 CTCTTTGGTTAAGAACATATCGCTATCCCAATTTAAATTCAGCAAGAGGAATCC 636
QY 652 TGCCAGGTTTAAACATCACT-----TGTACCTTCCACAAGACTCAGAACTCCAC 699
Db 637 TTCCACATACACACTACTTACCTCAAGTCGTGCATTAATGATGCTTAACAGAGATCCCT 696
QY 700 AGTGTCCCATTTTCCGACTAGAGACATCTTCCGAGAACACAGCGCATATTTTTCAGATG 759
Db 697 TCTGCCCATATATTCGCTCTTGCCAAATAGTGAGAACACGACACGGTTTCCAGGACA 756
QY 760 KSGCAATTGAGGGCGGATATGAGGCAATTCAGATCTACTGGGACTGCAACCTAGACCGTT 819
Db 757 TGGCGGTGAGGGAGGCAATGAGGCAATCCAGGTCACTGGGACTGCAACCTGAGCAGAG 816
QY 820 GGTTCATCACTGCGCTTCCCAATATACAGTTTTCCTCGCTTGAACAGAACACCAACG 879
Db 817 CGGCTTCCCTTGTGCTGCGAGGTACTCTTCCGCGCTCGATACAGGAGCTTGAGC 876
QY 880 TGTCCCTGACCTGGCTACAACTTACAGTACGCCAAGTACTACAGGAAACAAATG--- 936
Db 877 ACAACGTATCTCTGCTACAAATTCAGTTTTCGCAAGTACTACAGAGACCTGCTGGCA 936
QY 937 TTGAGAAACGGACTCTGATAAAGTCTTCGGGATCGTTTGACATCTGTTGGTATCTGGCA 996
Db 937 ACAGAGAGCGGACGCTATCAAGGCTTATGCGCTATGCGCTGACATATTTGTTGGGA 996
QY 997 CGGAGAGAAATTTGACATTTCCAGCTGGTTGTGATATCGGCTCAACCTCTCTACT 1056
Db 997 AGCAGGAGAAATTTGACATATCCCACTATCCCACTATGATCAATCGGCTGCGCTGCACTGC 1056
QY 1057 TCGGCTGCGGCTGTGTTTACGACTTCTCATC 1091
Db 1057 TAGGCATGCGGACCGCTGTGTGACATCATAGTC 1091

RESULT 5

US-08-750-134A-6
; Sequence 6, Application US/08750134A
; Patent No. 5985603
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,134A
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ. ID NO. 6:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1997 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-750-134A-6

Query Match 12.7%; Score 234.6; DB 2; Length 1997;
Best Local Similarity 55.5%; Pred. No. 4.4e-59;
Matches 585; Conservative 5; Mismatches 429; Indels 36; Gaps 6;

QY 55 TTTTCAGATGAGAGCAACAACTCGACTCGGATCCAGAGCATGAATATGCGACCACTTA 114
Db 135 TGTTCCAGTACGACACGCGCGCATCGTGTCTATCCGACCGCTAAAGTGGGGCTCATGA 194
QY 115 AGTGGTCTTCCAGCTGATCATCTTTTCCCTACG---TTTGGCTTTTCTGTGTGAGTGA 171
Db 195 ACCGCGGGTGCAGCTGCTCATCTGCTTACGTCATCGGTGGGTGGTGTGTTGGGAAA 254
QY 172 AGCTGTACAGCGGAAAGAGCTGTCTATCATAGTCTGTGCACACCAAGGTGAAGGGATAG 231
Db 255 AGGGCTACCAAGGAAACGGGACTCCGTTGGTCTAGCTCGGTGACACCAACCAAGGCTGTGG 314
QY 232 CAGAGGTGAAAGAGGAGATCGTGGAGATGGAGTGAAGAAGTTGGTGCACAGTGTCTTTG 291
Db 315 CTGTGACCAAC-----ACCTCTCAGCTTGGATTCGGGATCTGGGACGTGGCGGACTATG 368
QY 292 ACACCGCAGACTACACTTCCCTTTGAGGGGAACTCTTTTCTGTGTGATGACAAACTTTC 351
Db 369 TGATTCAG-----CTCAGGAGGAAACTCCCTCTTATTATGACCAACATGA 416
QY 352 TCAAAACAGAGGCCAAGAGCAGCGGTGTGTCCCGAGTATCCACCGCAGGACGCTCT 411
Db 417 TTGTACCGCTGACACAGACAGACAGACCTGTCCAGAGATCTCTGATAAGACCAACTTT 476
QY 412 GTTCTCTGACGAGGTGTATAAAGGATGGATGACCCGACAGAGCAAGGAATTCAGA 471
Db 477 GTAAATTCAGCGCGGACTGCTCTCTGCTCCGTCAGACACCCACAGCAGTGGGATTCGGA 536
QY 472 CCGGAGGTGTGTATRYATGAAGGGAACACAGAGACCTGTGAAGTCTCTCTCTCTGTCGC 531
Db 537 CTGGAAGATGTGTCTCTTCAATGAGTCTGTGAAGACTGTGAGGTGCTCATGTCGTCGC 596
QY 532 CCATTCAGGAGTGAAGAGCGCCCCCGGCTCTCTTTGAACAGTCCCGAAACTTCA 591
Db 597 CGGTGAGAACGACCTTGGCGTGGCAACGCGGCTTCTTAAAGGCTGCAGAAACTTCA 656
QY 592 CTGTGCTCTCAGAACATATCGACTTCCCGCGCCACACTACACACAGAGAAATCC 651
Db 657 CCTCTTGGTAAGAACACATCTGTGACCCCAAGTTTAACTTCAGCAAGAGGAATCC 716
QY 652 TGCCAGGTTTAA-----ACATCACTTGTACTCTCCACCAAGACTCA---GAATCCAC 699
Db 717 TCCCAACATCACCAGCTCTACCTCAATCTGCAATTTACATCTCTCAACGGATCCCT 776
QY 700 AGTGTCCCATTTCCGACTAGAGACATCTCCGAGAAACAGCGGATATTTTTCAGATG 759
Db 777 TCTGCCCATATTCGCTCTTGCCAAATCGTGGGGACCGCGGACATAGCTTCCAGGAGA 836
QY 760 KGGCAATTGAGGGCGGAAATATGGGCAATGAGATCTACTGGGACTGCAACCTAGACCGTT 819
Db 837 TGGCAGTTGAGGGAGGCAATGAGTATCCAGATCAAGTGGGACTGCAACCTGAGATAGAG 896
QY 820 GGTTCATCACTGCGCTCCCAATATACAGTTTTCCTCGCTTGAACAGAACACCAACG 879
Db 897 CGGCTTCCCTTGTGCTGCCAGATTTCTCTCGGCGCTGGACACCCCGGACCTGGAAC 956
QY 880 TGTCTTGTACCTGGCTACAACTTCAGATACGCCAAGTACTTACAGGA---AAACAATG 936
Db 957 ACAATGTGCTCTCTGCTTACATTTTCAGTTTCCCAAGTACTTACAGGAGCTGCGCGCA 1016
QY 937 TTGAGAAACGGACTCTGATAAAGTCTTCCGGATCGTTTGCATCTGCTGTTTGGCA 996

Db 1017 AAGAGCAGCGCACACTCACCAGGCGTAGGCGATCCGCTTGACATCATCGTGTGGAA 1076
Qy 997 CCGGAGGAAATTTGACATATCCAGCTGGTGTGTGACATCGCTCAACCCCTCTACT 1056
Db 1077 AGGCTGGAGAGTTTGTACATATCCCTTACCATGATCAACAGTGTGGCTTGGCTGGCGTCC 1136
Qy 1057 TGGGCTGGCCRCCTGTCTTCATCGACTTCCCTCATC 1091
Db 1137 TCGGGGTGGCAGCGTCTGTGAGGTCATAGTC 1171

RESULT 6

US-09-363-745-6
; Sequence 6, Application US/09363745
; Patent No. 6194162
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,745
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,134
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1997 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-363-745-6

Query Match 12.7%; Score 234.6; DB 4; Length 1997;
Best Local Similarity 55.5%; Pred. No. 4.4e-59;
Matches 585; Conservative 5; Mismatches 429; Indels 36; Gaps 6;

Qy 55 TTTTCCAGTATGAGACGACACAAAGTCACTCGATCCAGACATGAATATGSCACCATTA 114
Db 135 TGTTCAGTACGACACCGCGCATCGTCTCATCCGAGCGGTAAAGTGGGGCTCATGA 194
Qy 115 AGTGGTTCTCCACCTGATCATCTTTTCTCTAG--TTTGTCTTGTCTGTGAGTGACA 171
Db 195 ACCGCGCGGTGAGCTGCTCATCTGCTTACGTATCGGTGGGTGTTCTGTTGGGAAA 254
Qy 172 AGCTTACGACGGGAAAGAGCTGTGATCATCTGTGACACACCAAGGTGAAGGGGATAG 231
Db 255 AGGGCTACCGAGAAAGAGTCCCGTGTGCTGAGCTCGTGCACACCAACCAAGGTGG 314
Qy 232 CAGAGTGAAGAGAGATCGYGGAATGGAGTGGAGTGGTGGTGCACATGCTCTTG 291

Db 315 CTGTGACCAAC-----ACCTCTCAGCTTGATTCGGATCTGGGACGTGGCGGACTATG 368
Qy 292 ACACCGCAGACTACACCTTCCCTTTGAGGAGAACTTCCTTCTGATGACAAACTTTC 351
Db 369 TGATTCAG-----CTCAGGAGGAAAACTCCCTCTTCATTATGACCAACATGA 416
Qy 352 TCAAAACAGAAAGCCCAAGAGCAGGGTGTGTCCTCCAGTATCCACCGCGAGGAGCTCT 411
Db 417 TTGTCACCGTGAACACAGACAGACACCTGTCCAGAGATCTCTATAGACCAAGATTT 476
Qy 412 GTTCTCTGACCGAGGTGTGTAAGAGGATGATGAGACCGCAGAGCAAGAAATTCAGA 471
Db 477 GTATTCAGACGCGGACTGCACTCTGCTCGGTGGACACCCACAGCAGTGGCTTCGA 536
Qy 472 CCGAAGGTGTGTAGTATGAGGAAACAGAGACCTGTGAAGTCTCTGCTTGGTGGCC 531
Db 537 CTGGAAGATGTGCTTCTTCAATGAGTCTGTGAGAGCTGTGAGGTGGCTCATGTGGTCC 596
Qy 532 CCATCGAGGAGTGGAGAGGCCCCCGGCTGCTCTTGAACAGTCCGAAACATTCGA 591
Db 597 CGTGGAGAGACGCTGTGGCTGCCACACGCGGCTTCTTAAAGCTCGAGAAACTTCA 656
Qy 592 CTGTCTCATCAAGAAATATCGACTTCCCGGCGCAACTACACACAGAGAAACATCC 651
Db 657 CCTCTGTGTAAGAAACAATCTGGTACCCCAAGTTTAACTTCAGCAAGAGAAACATCC 716
Qy 652 TCCAGGTTTAA-----ACATCACTTGACTTCCACAGACTCA---GAATCCAC 699
Db 717 TCCCAACATCACACGCTCTTACCTCAATGCTGATTTACATGCTCAACGGATCCCT 776
Qy 700 AGTGTCCATTTTCCGACTAGGAGACATCTTCCGAGAAACAGCGCATATTTTCAGATG 759
Db 777 TCTGCCCATATTCGGTCTTGGCAATCTGGGGGACGCGGACATAGCTTCCAGGAGA 836
Qy 760 KGGCAATTCAGGGGGAATAATGGGCATGAGATCTACTGGSACTGCAACCTAGACCGTT 819
Db 837 TGGCAGTTGAGGGAGCATCTGGGTATCCAGATCAAGTGGGACTGCAACCTGGATAG 896
Qy 820 GGTTCATCACTGCTCCCAATACAGTTCCCTGCGCTTACGACAGACAGACCACCAAG 879
Db 897 CGGCTCCCTTGGCTGCCAGATATTTCTTCGGCGCTTGGACACCCCGGACCTGGAC 956
Qy 880 TGTCTTGTACCTGGCTACAACTTCAATCAGATCAGCCAGTACTACAAGGA---AAACAATG 936
Db 957 ACAATGTCTCTCTGGCTACAATTTCAAGTTTGGCAAGTACTACAGGAGACCTGGCGGCA 1016
Qy 937 TTGAGAAACGAGCTCTGATAAAGTCTTCGGGATCCGTTTGTGACATCTGTTTGGCA 996
Db 1017 AAGACGCGCACACTCCACAAAGCGGTACGGCATCCGCTTGGACATCATCGTGTGGAA 1076
Qy 997 CCGGAGGAAATTTGACATATCCAGTGGTGTGTGTATCGCTCAACCTCTCTACT 1056
Db 1077 AGGCTGGGAGTTTGACATCATCCCTACCATGATCAAGTTGGCTCTGCTGGCGCTCC 1136
Qy 1057 TCGGTCTGCGCCTGTGTGTATCGACTTCTCTATC 1091
Db 1137 TCGGGGTGGCAGCGTCTGTGTGAGTCAATAGTC 1171

RESULT 7

US-08-750-134A-10
; Sequence 10, Application US/08750134A
; Patent No. 5985603
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA

```

Db      1023  A-----AFTCTCCCCAGGCTCAACTTCAGGTTGTCGAGGCACATTGTGGAGAAC 1071
QY      933  AATGTTGAGAAACGGACTCTGATAAAAGCTTTCGGGATCCGTTTTCACATCCTCGTGTIT 992
Db      1074  GGGACCAACTACCGTCACTCTTCAGAGTGTGTTGGATTCGCTTGACATCCTCGTGGAC 1133
QY      993  GGCACCGGAGGAAATTTGACATATTCAGCTGGTGTGTGTACATCGGCTCAACCTCTCC 1052
Db      1134  GGCAGCGCGGGAAGTTTGCATCATCCCTACAAATGACCACTCGCTCTGGAATTGGC 1193
QY      1053  TACTTCGGTCTGGCCRCGTGTTCATCGACTTCCT 1087
Db      1194  ATCTTTGGGTGGCCACAGTTCTCTGTGACCTGCT 1228

RESULT 8
US-09-363-745-10
; Sequence 10, Application US/09363745
; Patent No. 6194162
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,745
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,134
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2643 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-363-745-10

Query Match 11.0%; Score 203.8; DB 4; Length 2643;
Best Local Similarity 54.8%; Pred. No. 6.5e-50;
Matches 447; Conservative 5; Mismatches 342; Indels 21; Gaps 2;

QY      295  GTCTTTTCACCGCAGACTACACTTCCTTCCTTCAGGGGAGACTCTTTCTTCGTGATGACA 344
Db      423  GTCTGGGATGTGGCTGACTAGCTTCCACGCCAGGGGAGACCTCTTCGTGTGTCATG 482
QY      345  AACTTTCTCAAAACAGAGGCCAAGAGCAGCGGTTGTCTCCCGAGTATCCACCCGACGG 404
Db      483  ACCAATTTTATGCTGACCCCGAGCAGACTCAGGCTACTCCGCAGAGCACCCAGAAGG 542
QY      405  ACGTCTGTTCCTTCGACCGCAGGTTGTAAAGAGGATGGATGACCCCGCAGACGAAAGGA 464

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Db 543 GGCATATCAAGAGGACAGCTGGCTGTACCCCTGGGAGGCCAAGAGGAGGCCCAAGGC 602
QY 465 ATTCAGACCGGAGGTGTGTAGTATATGAAGGAAACAGAGACCTGTGTGAAGTCTCTGCC 524
Db 603 ATCCGACGCGGACAGTGTGGCCCTTCAACGACACTGTGAAGACGTGTGAGATCTTTGGC 662
QY 525 TGGTCCCATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 584
Db 663 TGGTCCCGGTGGAGGTGTGATGACGACATCCGCGGCGCTGCCCTTCCGAGAGCGGAG 722
QY 585 AACTTCACTGTCTATCAAGAGAAATATGACATTCCTCCGCGGAGGAGGAGGAGGAGGAG 644
Db 723 AACTTCACTCTTTTCAACAGACAGACACTTCCAGCTTCAAGCTCAACAGGAGGAG 782
QY 645 AACTTCACTCTTTTCAACAGACAGACACTTCCAGCTTCAAGCTCAACAGGAGGAG 692
Db 783 AACTTCACTCTTTTCAACAGACAGACACTTCCAGCTTCAAGCTTCAACAGGAGGAG 842
QY 693 AATCCACAGTGTCCCATTTCCGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 752
Db 843 CACCCGCTGTCCGAGCTTCCAGCTTGGCTACGTTGGTGTGCAAGTGTGAGGAGGAG 902
QY 753 TCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 812
Db 903 AGCAGCTGGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 962
QY 813 GACCGTGTGTTTCCATCACTGCTCCGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 872
Db 963 GACTGGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1022
QY 873 ACCAAGTGTCTTGTACCTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 932
Db 1023 A-----ATCTCTCCGAGGCTTCACTTCAAGTGTGAGGAGGAGGAGGAGGAGGAG 1073
QY 933 AATGTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 992
Db 1074 GGGACCAACTACCGTCTCAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1133
QY 993 GGCACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1052
Db 1134 GGCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1193
QY 1053 TACTTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1087
Db 1194 ATCTTGGGGTGGCCACAGTCTCTGTGAGCTGCT 1228
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RESULT 9

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US-08-750-134A-4
; Sequence 4, Application US/08750134A
; Patent No. 5985603
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,134A
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1837 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: rat P2x from vas deferens
; US-08-750-134A-4
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Query Match 8.6%; Score 159.6; DB 2; Length 1837;
Best Local Similarity 50.7%; Pred. No. 5.8e-37;
Matches 434; Conservative 6; Mismatches 395; Indels 21; Gaps 2;

QY 244 AGGAGATCGYGGAGAAATGGAGTGAAGAAAGTTGGTGCACAGTGTCTTTGACACCCGAGACT 303
Db 418 AGGGCTTGGCTGTGACCCAGCTCCAGGGCTCCAGGAGCCAGGAGTCTGGGACGTGGCTGACT 477
QY 304 ACACCTTCCCTTTCAGGGGAACTCTTCTTCGTGTGATGACAAACACTTCTCAAAAACAGAG 363
Db 478 ATGCTTCCACAGACAGGGGAGACTCTCTTTGTAGTTATGACCAACTTCATCGGTGACCC 537
QY 364 GCCAAGAGCAGCGGTGTGTCCCGAGTATCCACCCGAGGAGCGTCTGTCTCTGACCC 423
Db 538 CTCACGACACTCAAGGCCATTTGTGCAGAGAACCCAGAGGTGSCATATCCAGGATGACA 597
QY 424 GAGGTGTAAAGAGGATGGATGGACCCGACAGACAAAGAAATTCAGACCCGAGAGGTGTG 483
Db 598 GTGGTGTCACTCCAGGAAAGAGAAAGAAAGGAAAGGATTCGCACAGGCAACTGTG 657
QY 484 TAGTGTATGAGAGGAAACCCAGAGAGACTGTGAGTCTCTGCTGTGTCGCCCTCCAGGCGAG 543
Db 658 TCCCTCTCAATGGCAGTGTGAGAGACATGTGAGATCTTTTGGTGTCTCTGTAGAGGTGG 717
QY 544 TGAAGAGCGCCCGCCCTGTCTCTTGAACAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAG 603
Db 718 ATGACAAGATCCCAAGCCCTGTCTCTTCTGAGGCTGAGACTTCACCTCTTCTATCA 777
QY 604 AGAACATATGACTTCCCGGCGCAACTACACACAGAGAAACATTCCTGCGAGGTTAA 663
Db 778 AAAACAGCATCAGCTTCCACGCTTCAAGGTCAACAGGCGCAACCTGTGTAGAGGAGTGA 837
QY 664 ACATCAGCTTGA-----CCTTCCACAGACTCAGATCCACAGTGTCCCATTT 711
Db 838 ACGGACCTACATGAAGAAGTGCCTCTATCACAGATTCACACCCCTGTGCGCGTCT 897
QY 712 TCCGACTAGGAGACATCTTCCGAGAAACAGCGGAGTAAATTTTCAGATGKGGCAATTCCAGG 771
Db 898 TCAACCTTGGCTATGTGTGCGAGAGTCAAGGAGGAGTCCCGAGGCTTCCGAGGAGG 957
QY 772 GCGGAATAATGGGCAATTGAGATCTACTGGGACTGCAACCTTAGACCGTGTGTTCCATCACT 831
Db 958 GTGGGTGGTGTGATCAACATGACTGGAAGTGTGATCTGGACTGGCAGCTTCCGCACT 1017
QY 832 GCGTCCCAATACAGTTCCTCGCTGCTGAGCAGACAGACCCACAGCTGTCTGTGAC 891
Db 1018 GCAAAACCATCTACCAAGTTCACGAGCTGTATGGGAGAGAAACC-----TGCTC 1068
QY 892 CTGGCTACACTTCAGATACGCGCAAGTACTACAGGAGAAACATTTGTGAGAAAGGACTC 951
Db 1069 CAGGCTTCACTTCAGATTTGCCAGGATTTCTGTGAGATGGGACAAACCGTGTGTCAC 1128
QY 952 TGATATAAGTCTTGGGATCCCGTTTGTGATTCCTGAGTGTGTTGGCAACCGGAGAAATTTG 1011
Db 1129 TCTTCAAGTGTGTGGGATTCACCTTTGATATCTCTTGTGATGCAAGGAGGAGTGTG 1188
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; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequencing Primer
US-09-191-136-13

Query Match      8.0%; Score 148.4; DB 4; Length 1272;
Best Local Similarity 54.8%; Pred. No. 9,4e-34;
Matches 362; Conservative 3; Mismatches 274; Indels 21; Gaps 3;

QY 461 AGAANTCAGACCGGAGGTGTGTAGTATGAAGGAACCAAGAGACCTGTGAGTCTC 520
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Db 557 AGGATCTCTACTGCGCGTGTGTAATACAGCTGTGCTCCGGAAGCTGTGAGATCCA 616

QY 521 TGCCTGTGTCCTCATCAGGAGCTGGAAGAGCCCGCCGCTCTCTTTGACAGTGC 580
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Db 617 GGGCTGGGCGCCCGAGGAGTGACACAGTGTGAAGCGC-----CCATCATGTGGAAGC 670

QY 581 CGAAACTTCACTGTCTCATCAAGAACAATATCGACTTCCCGGGCCCAACTACACAC 640
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Db 671 TGAGAACTTCACTATTTTCATCAGACAGCATCGCTTTCCCGCTTCACTTTGAGAA 730

QY 641 GAGAAATCTTCCAGGTTTAAACATC-----ACTGTACCTTCCACAGAC 688
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Db 731 GGGAAACCTCTTCCCAACCTGACAGCCAGGAGCATGAAGACCTGCGCTTCCACCGGA 790

QY 689 TCAGAAATCCACAGTGTCCCATTTTCGACTAGGAGACATCTCCGAGAAACAGGCGATA 748
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Db 791 CAGGAGACCTTTTACCCCATCTTGGCGGTAGGGAGCTGGTCAAGTTGGCGGGCAGGA 850

QY 749 TTTTTCAGATGKGCAATTCAGGGCGGAATATGGGCAATGAGATCTACTGGGATGCAA 808
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QY 869 GACCAACCACTGTCTTGTACCTTGTACAACTTCAGATACGCCAAGTACTACAA--- 925
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QY 986 GGTTTTGGACCGGAGAAATTTGACATTAATCCAGCTGGTGTGTATACGCGCTCAAC 1045
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Db 1091 GGTATACGGGAATCTGGCAAGTTCACATCATCCCAACCATCATCAGCTCTGTGGCGGC 1150

QY 1046 CCTCTCTACTTCTGCTGCGCCCTGTGTTCATCGACTTCTCATCGACASTTACTCCAG 1105
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Db 1151 CTTTACTTCTGTGGAGTGGGACGTCTCTGTGATCATCTCTCTCACTTCTCTCAG 1210

RESULT 12
US-09-191-136-15
; Sequence 15, Application US/091911368
; Patent No. 6214581
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Lynch, Kevin J.
; APPLICANT: Burgard, Edward C.
; APPLICANT: Van Biesen, T.
; TITLE OF INVENTION: Nucleic Acids Encoding A Functional
; TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
; TITLE OF INVENTION: And Use Thereof
; FILE REFERENCE: 6293.US.P1
; CURRENT APPLICATION NUMBER: US/09/191,136B
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: US 09/008,526
; EARLIER FILING DATE: 1998-01-16

; EARLIER APPLICATION NUMBER: US 09/008,185
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 60/071,298
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 60/071,669
; EARLIER FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1243
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-191-136-15

Query Match      8.0%; Score 148; DB 4; Length 1243;
Best Local Similarity 54.9%; Pred. No. 1.2e-33;
Matches 361; Conservative 3; Mismatches 273; Indels 21; Gaps 3;

QY 462 GGAATTCAGACCGGAAGTGTGTACTRYATGAAGGAACCAAGAGACCTGTGAAGTCTCT 521
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QY 522 GCCTGGTGGCCCATCATCAGAGCAGTGGAGAGCCCGCCGCTCTCTTTGAACAGTGCC 581
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QY 582 GAAAACTTCACTGTCTCATCAAGAACAAATATCGACTTCCCGGGCCCAACTACACCAAG 641
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QY 642 AGAAACATCTCTGCGAGGTTTAAACATC-----ACTGTACCTTCCACAGACT 689
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Db 598 GGAACACTCTCTTCCAACTGACACCCAGGAGCATGAAGACCTGCCGCTTCCACCCGAC 657

QY 690 CAGAAATCAAGTGTCCCATTTTCGACTAGGAGACATCTTCGAGAAACAGAGCGATAAT 749
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Db 658 AAGGACCTCTTCTGCCCCATCTTGGGGTAGGGAGCTGGTCAAGTTTTCGGGACAGGAT 717

QY 750 TTTTTCAGATGKGCAATTCAGGGCGGAATATGGGCAATGAGATCTACTGGGACTGCAAC 809
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Db 718 TTTGCCAACTGGCGGCGACGGGGAGTTCTGGGCATTAAGATCGGTGGGTGTGGCAG 777

QY 810 CTAGACCTTGGTGTTCATCATCTCCCTCCCAATACAGTTTCCRTCCGCTTGAAGACAAG 869
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Db 778 TTGGACAGAGCGCTGGGACAGTGCATCCCAATACCTTCCACCCGCTCGACAGCGTT 837

QY 870 ACCACCAAGTGTCTTGTGACCTGGCTACAACTTCAGATCAGCAAGTACTACAA---G 926
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QY 927 GAAACAAATGTGAGAAAGGAGCTCTGATAAAGCTTTCGGGATCCGTTTGGACATCTG 986
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Db 898 GAAATGCGAGTGAATACCGACCTCTCTGAGGCTTTTGGCATCCGCTTGGAGTCTG 957

QY 987 GTTTTGGACCGGAGAAATTTGACATTAATCAGCTGGTGTGTATACGCGCTCAACC 1046
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Db 958 STATACGGGAATGCTGCAAGTTCAACATCATCCCAACCATCATCAGCTCTGTGGCGGC 1017

QY 1047 CTCCTCTACTTCTGCGCTGCGCTGTGTTCATGCTCTCTCATCGACASTTACTCCA 1104
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Db 1018 TTTACTTCTGTGGAGTGGGAATCTTCTCTGTGACATCATCTCTGCTCAACTTCTCA 1075

RESULT 13
US-08-750-134A-8
; Sequence 8, Application US/08750134A
; Patent No. 5985603
; GENERAL INFORMATION:
; APPLICANT: VALEIRA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 20:13:22 ; Search time 2709 Seconds
(without alignments)
11077.976 Million cell updates/sec

Title: US-09-977-221-2-C-AT-1513

Perfect score: 1853

Sequence: 1 aaacacgaggaggagct.....cgtctgtaatccacatttt 1853

Scoring table: IDENTITY_NVC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1635	88.2	3013	11	BC007679	Homo sapi
2	674	36.4	795	13	BI861622	603390486
3	671.8	36.3	946	12	BF347747	602022388
4	666.8	36.0	937	12	BF68165	602744202
5	645.4	34.8	932	13	BI603534	603244436
6	613.8	33.4	769	12	BG766449	602739207

7	564	30.4	860	13	BI598073	
8	553.8	29.9	841	12	BG769595	
9	547.4	29.5	908	12	BF689446	
10	498.6	26.9	817	10	BE382829	
c	11	486.4	1022	12	BF690388	
12	430	23.2	543	12	BF347290	
13	399.6	21.6	642	14	BQ554327	
14	390.2	21.1	783	12	BG769470	
15	373	20.1	555	12	BF347097	
16	288.6	15.6	475	10	BE689531	
17	246.2	13.3	247	9	AA210664	
18	237	12.8	1844	11	BC017458	
19	235.6	12.7	368	10	BE448796	
20	225.2	12.2	1992	11	BC002099	
21	211.8	11.4	910	14	BQ681359	
22	210.2	11.3	937	13	BI687408	
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24	201	10.8	867	14	BQ888542	
25	200.6	10.8	844	9	AJ446359	
26	191.6	10.3	659	10	AW913237	
27	186.4	10.2	1051	9	AL544542	
28	182.2	9.8	595	13	BI536809	
29	181.8	9.8	244	9	AA672571	
30	181.6	9.8	581	13	BI681932	
31	181	9.8	331	10	AW899099	
32	178.4	9.6	753	13	BI452907	
33	178.4	9.6	847	9	AJ445426	
c	34	168.2	9.1	261	12	BF928435
c	35	166.6	9.0	454	9	AI962024
36	161	8.7	276	9	AA362346	
c	37	160.6	8.7	644	10	AW975596
38	156.2	8.4	1059	14	BM919221	
39	156	8.4	1009	13	BM459621	
40	152.2	8.2	903	9	AL541451	
c	41	150	8.1	416	9	AA713768
c	42	150	8.1	488	10	BE626188
c	43	149.8	8.1	494	10	BE178695
c	44	148.6	8.0	497	10	BE690562
45	147.8	8.0	924	9	AL550650	

ALIGNMENTS

RESULT 1	BC007679	3013 bp	mRNA	linear	HTC 12-JUL-2001
LOCUS	Homo sapiens, Similar to purinergic receptor P2X, ligand-gated ion channel, 7, clone IMAGE:3628076, mRNA.				
DEFINITION	Homo sapiens, Similar to purinergic receptor P2X, ligand-gated ion channel, 7, clone IMAGE:3628076, mRNA.				
ACCESSION	BC007679				GI:14712732
VERSION	BC007679.1				
KEYWORDS	HTC.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 3013)				
AUTHORS	Strausberg,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgaps-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; web site: http://www.nisc.nih.gov/				

Contact: nisc_mgcen@hgrl.nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
 Lim, M., Maduro, Q.L., Masello, C., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
 Tionson, E.E., Touchman, J.W., Teurigne, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 12 Row: g Column: 6
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4505552
 This clone has the following problem: incomplete processing.

FEATURES
 Location/Qualifiers

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 /db_xref="taxon:9606"
 /clone="IMAGE:3628076"
 /tissue_type="Brain, neuroblastoma"
 /clone_lib="NHL MGC_19"
 /lab_host="DH10B-R"
 /note="Vector: pORF"

BASE COUNT 792 a 781 c 752 g 688 t

ORIGIN

Query Match 88.2%; Score 1635; DB 11; Length 3013;

Best Local Similarity 93.9%; Pred. No. 0;

Matches 1736; Conservative 13; Mismatches 3; Indels 97; Gaps 1;

QY 5 CGCAGGAGGAGGCTGCACATCGCGGCTGCTGCAGCTGCAGTGCATGTTTCCAGTA 64
 DB CCGCAGGAGGAGGCTGCACATCGCGGCTGCTGCAGCTGCAGTGCATGTTTCCAGTA 88
 QY 65 TGAGACGACAAAGTCACTCGGATCCAGACATGAAATATGCGACCAATTAAGTGTTCT 124
 DB TGAGACGACAAAGTCACTCGGATCCAGACATGAAATATGCGACCAATTAAGTGTTCT 148
 QY 125 CCAGTGATCATCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 184
 DB CCAGTGATCATCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 208
 QY 185 GAAAGACCTGTCATCAGTCTTCTGACACACCAAGTGAAGGGATAGCAGAGTGAAGA 244
 DB GAAAGACCTGTCATCAGTCTTCTGACACACCAAGTGAAGGGATAGCAGAGTGAAGA 268
 QY 245 GGAGATCGGGAGATGAGTGAAGAGTGGTGACAGTGTCTTTGACACCCAGACTA 304
 DB GGAGATCGGGAGATGAGTGAAGAGTGGTGACAGTGTCTTTGACACCCAGACTA 328
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 QY 365 CCAGAGCAGCGGTGTGTCGCCAGTATCCACCCGAGGACGCTGTCTTCTTCTGACG 424
 DB CCAGAGCAGCGGTGTGTCGCCAGTATCCACCCGAGGACGCTGTCTTCTTCTGACG 448
 QY 425 AGTTTGTAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
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 QY 545 GGAGAGGCCCCCGGCTGTCTTCTTGAACAGTCCGAAACTTCTACTGTGCTCATCAA 604
 DB GGAGAGGCCCCCGGCTGTCTTCTTGAACAGTCCGAAACTTCTACTGTGCTCATCAA 531
 QY 605 GAACAATATGACTTCCCGGCACACTACACCGAGACATCTGCTCCAGGTTTAA 664
 DB GAACAATATGACTTCCCGGCACACTACACCGAGACATCTGCTCCAGGTTTAA 1671

DB 532 GACAAATATCGACTTCCCGCCACAACTACACACAGAGAAACATCTGCCAGGTTTAA 591
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 DB CTCTCAGCCTGTGTGTTGCTCAAGAACTACTACTACAGGAAAGTGGAGTGCATTTG 1131
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 DB GCTKGGCTGATGTGATTCACCAAGCCGCTGCGGCGACTGTGCTTCCAGGTCGA 1611
 QY 1685 CGCCACTGGGCTTCCGCTCCAGGACATGCTGACTTTGCCATCTTCCAGCTGCTG 1744
 DB CGCCACTGGGCTTCCGCTCCAGGACATGCTGACTTTGCCATCTTCCAGCTGCTG 1671

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QY 1745 CCGTGGAGGATCCGGAAGAGTTTCRAAGAGTGAAGGCGAGTACAGTGGCTCAAGAG 1804
Db 1672 CCGTGGAGGATCCGGAAGAGTTTCRAAGAGTGAAGGCGAGTACAGTGGCTCAAGAG 1731
QY 1805 TCCTTACTGAAGCAGGACCGCTGGCTCAGCTGTGTAATCCACGCTTTT 1853
Db 1732 TCCTTACTGAAGCAGGACCGCTGGCTCAGCTGTGTAATCCACGCTTT 1780

RESULT 2
BI861622 795 bp mRNA linear EST 10-OCT-2001
LOCUS 603390486F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5399565 5',
DEFINITION mRNA sequence.
ACCESSION BI861622
VERSION BI861622.1 GI:16002369
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 795)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM2018 row: k column: 22
High quality sequence stop: 772.
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            Note: this is a NIH_MGC Library."
BASE COUNT 176 a 231 c 228 g 160 t
ORIGIN

Query Match 36.4%; Score 674; DB 13; Length 795;
Best Local Similarity 97.7%; Pred. No. 7.2e-171;
Matches 707; Conservative 7; Mismatches 7; Indels 3; Gaps 3;

QY 1116 CGCTCCCATATTTATCCCTGGTGCAGTGTCTGCAGCCCTGTGGTCAAGATATAC 1175
Db 1 CGCTCCCATATTTATCCCTGGTGCAGTGTCTGCAGCCCTGTGGTCAAGATATAC 60

QY 1176 TACAGGAAGAGTGCAGTCCATTGTGGAGCAAGCCGACATTAAGTATGTCTCTT 1235
Db 61 TACAGGAAGAGTGCAGTCCATTGTGGAGCAAGCCGACATTAAGTATGTCTCTT 120

QY 1236 GTGGATGAATCCACATTAAGTATGTGGAGCAAGCCGACATTAAGTATGTCTCTT 1295
Db 121 GTGGATGAATCCACATTAAGTATGTGGAGCAAGCCGACATTAAGTATGTCTCTT 180

QY 1296 GTCAGGGCCAGAGTCCSAGACCTGATGGACTTCACAGATTGTCCAGGCTGCC 1355
Db 181 GTCAGGGCCAGAGTCCSAGACCTGATGGACTTCACAGATTGTCCAGGCTGCC 240

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QY 1356 CTGCGCTCCATGACACACCCCGGATTCCTGGACCAACAGAGGATACRGCTGCTTAGA 1415
Db 241 CTGCGCTCCATGACACACCCCGGATTCCTGGACCAACAGAGGATACRGCTGCTTAGA 300
QY 1416 AAGGAGCGGACTCCTAGATCCAGGATAGCCCTGTCTGGTGCAGTGTGGAGTGCCTC 1475
Db 301 AAGGAGCGGACTCCTAGATCCAGGATAGCCCTGTCTGGTGCAGTGTGGAGTGCCTC 359
QY 1476 CCATCTCAACTCCCTGAGGCGCAGAGTGCCTGGAGGCGCTGTGCTCCGGAAGACCG 1535
Db 360 CCATCTCAACTCCCTGAGGCGCAGAGTGCCTGGAGGCGCTGTGCTCCGGAAGACCG 419
QY 1536 GGGCGCTGCATACACCACTCAGAGTGTTCAGGAAGTGTCTCTGTCAGACAGTCTGTG 1595
Db 420 GGGCGCTGCATACACCACTCAGAGTGTTCAGGAAGTGTCTCTGTCAGACAGTCTGTG 479
QY 1596 CAGTTCCTCCTGCTCTACAGGAGCCCTGTGCTGGCGCTGGATGTGGATTCACCAACAGC 1655
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QY 1656 CGGTGCGGCGACTGTCCCTACAGTGTACAGGAGTGTACAGGAGTGTGGCTTCCGAGCATG 1715
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QY 1716 GCTGAC-TTTGGCATTCTCCCGAGCTGTGCTGGAGGATCCGGAAGAGTTTCCRAA 1774
Db 600 GCTGAC-TTTGGCATTCTCCCGAGCTGTGCTGGAGGATCCGGAAGAGTTTCCRAA 659
QY 1775 GAGTGAAGGCGAGTACAGTGGCTTCAAGAGTCC-TTACTGAAGCCAGCAGCCGCTGGCTCA 1833
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QY 1834 CGTC 1837
Db 720 CGTC 723

RESULT 3
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DEFINITION 5', mRNA sequence.
ACCESSION BF347747
VERSION BF347747.1 GI:11295342
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/lab_host="DH10B (phage-resistant)"
Note="Organ; skin; Vector: pOB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 198 a 189 c 215 g 167 t
ORIGIN
Query Match 33.4%; Score 619.8; DB 12; Length 769;
Best Local Similarity 95.2%; Pred. No. 3.2e-156;
Matches 690; Conservative 3; Mismatches 25; Indels 7; Gaps 5;
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DB 169 CCACGTGATCACTTTTCCACGTTTGTCTTCTGCTGAGTGACAGAGTGTACACGG 228
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QY 245 GGAGATCGGAGAGTGAAGTGAAG-GAAGTGTGTCACAGTCTTTTGACACCGAGACT 303
DB 289 GGAGATCGGAGAGTGAAGTGAAGGAGCCTGTGTGCAGAGTGTGTGACACCGAGACT 348
QY 304 ACACCTTCCTTTGAGGGGAACTCTTCTGCTGATCAAACTTCTCA-AAACAGAA 362
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QY 363 GGCCAAAGACGCGGTTGTGTCGAGTATCCACCCGAGGAGCCTCTTCTCTGAC 422
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QY 423 CGAGGTTTAAAGGGATGGATGGAGCCCGCAGAGCAAGGAATCAGACCGGAGGTGT 482

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469 CCAGGTTTAAAGGGATGGATGGAGCCCGCAGAGCAAGGAATCAGACCGGAGGTGT 528
QY 483 GTAGTATATGAAGGGAACCAAGACCTGTGAAGTCTCTCTCTGCTGTCGCCATCGAGCA 542
DB 529 GTAGTATATGAAGGGAACCAAGACCTGTGAAGTCTCTCTCTGCTGTCGCCATCGAGCA 587
QY 543 GTGAGAGAGGCCCCCGGCTCTCTCTGTCGACAGTCCGAAAACCTCACTGTGCTCATC 602
DB 588 GGG---AAGAGGCCCCCGGCTCTCTCTGTCGACAGTCCGAAAACCTCACTGTGCTCATC 644
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QY 663 ACATCACTTTGATC-TTCCACAGACTCAAGATCCACAGTGTCCCATTTTCCGACTAGG 721
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DEFINITION BI598073.1 GI:15491012
ACCESSION BI598073
VERSION BI598073.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L16M1769 row: p column: 01
High quality sequence stop: 711.

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); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',
size selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI), National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 223 a 211 c 239 g 187 t
ORIGIN
Query Match 30.4%; Score 564; DB 13; Length 860;

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112	CGCAGGAGGAGGCGTGCACATGCGCGGCGCTGCAGCTGCAGTGCAGTATTTCCAGTA	171							
65	TSAGACGAACAAGTCACTCGGATCCAGACAGATGAATATGGCACCATAAAGTGGTCTT	124							
172	TSAGACGAACAAGTCACTCGGATCCAGACAGATGAATATGGCACCATAAAGTGGTCTT	231							
125	CCACGTGATCACTTTTCTGAGTTGCTTTCGTGAGTGACACAGCTGTACACAGG	184							
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185	GAAGAAGCCTGTCTGTCGACACCAAGGTGAAGGGATGACAGAGGTGAAGA	244							
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352	GGAGATCGTGGAGATGGAGTGAAGAAGTTGGTGACACAGTCTCTTTGACACCCGACACTA	411							
305	CACCTTCCCTTTTCGAGGGGAAGTCTTTCCTGCTGATGACAAACTTCTCAAAACAGAGG	364							
412	CACCTTCCCTTTTCGAGGGGAAGTCTTTCCTGCTGATGACAAACTTCTCAAAACAGAGG	471							
365	CCACAGACAGCGGTGTGTGCCGAGTATCCACCCGACAGGAGCTCTGTCTCTCTGACCG	424							
472	CCACAGACAGCGGTGTGTGCCGAGTATCCACCCGACAGGAGCTCTGTCTCTCTGACCG	531							
425	AGGTTGTAAAA-AGGGATGGATGGACCCGACAGCAAGAAGATTCAGACCGGAAGTGTG	483							
532	AGGTTGTAAAAAGGAGATGGATGGACCCGACAGCAAGAAGATTCAGACCGGAAGTGTG	591							
484	TAGTATATGAAGGAACACAGAGACCTG-TGAAGTCTCTGCTGTGTGCCCC-ATCGAGGC	541							
592	TAGTATATGAAGGAACACAGAGACCTG-TGAAGTCTCTGCTGTGTGCCCCAATTCGAGGC	651							
542	AG--TGGGAAGAGCCCCCGGCGCTG-CTCTCTTGAACAGTGGCGAAAAACTTCAGTGTCT	598							
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599	CATCAAGACAATATGCACTTCCCGGCGCAACTTACACACAGAGAAACATCCCTGC	654							
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DEFINITION					mRNA sequence.
ACCESSION	BG769595				
VERSION	BG769595.1	GI:14080248			
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SOURCE	human.				

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REFERENCE	Bumkayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 841)
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: AFCC/DCD/DTF cDNA library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

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BASE COUNT	224 a	202 c	237 g 178 t
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QY	185	GAAGAGCCGTGCATCAGTCTGTGTCACACCAAGGTGAAGGGATGACAGAGTGAAGA	244
DB	230	GAAGAGCCGTGCATCAGTCTGTGTCACACCAAGGTGAAGGGATGACAGAGTGAAGA	289
QY	245	GGAGATCGYGGGAATGGAGTGAA--GAAGTTGGTGTCACAGTGTCT--TTTGACACCGCAG	302
DB	290	GGAGATCGTGGGAATGGAGTGACAGAGAGTGTGTGTCACAGTGTCTTTTGACACCGCAG	349
QY	303	TACACCTTCCTTTTGCAGGGAACTTTCTTCTGATGACAAACTTTCTCAAAA--CAGA	361
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QY	362	AGGCCAAGACAGCGGTGTCT--GTCCAGATGCCACCGCAGAGAGCG--TCTGTCTCTCT	419
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QY	420	GACCGAGGTGTGA--AAAAAGGATGATGGACCCGACAGCAAGGAATTCAGACCGGAAG	478
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QY	479	GTGTGTAGTATGTAGAGGAACACAGAACTGTGAA--GTCTCTGCTGGTGGTCCCATC	536
DB	529	GTGTGTAGTATGTAGAGGAACACAGAACTGTGAA--GTCTCTGCTGGTGGTCCCATC	588
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DB	589	GAGCAGTGTGAAGGGCCCCCGGGGCTGGTCTCTTTGAACAGTGCAGAAACTTTCACGT	648
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 VERSION BE689446.1 GI:11974854
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 908)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCMD/DTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 plate: LLCM1155 row: c column: 04
 High quality sequence stop: 668.
 Location/Qualifiers
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 EcoRI; cDNA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library. |"
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 817)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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 /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GSCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit

RESULT 11	BF690388	1022 bp	linear	EST 22-DEC-2000
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VERSION	BF690388.1	GI:11975796		

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ACCESSION	BF690388			
VERSION	BF690388.1	GI:11975796		

Query Match	26.2%;	Score 486.4;	DB 12;	Length 1022;
Best Local Similarity	95.0%;	Pred. No. 4.1e-120;		
Matches 496;	Conservative 5;	Mismatches 21;	Indels 0;	Gaps 0;
QY	1332	TTCCAGATTGTTCAGAGCTGCCCTGGCCCTCCATGACACACACCCGATTCCTGGACAA	1391	
Db	715	TTCCAGACCTTGTCTCCAGCTGCCCTGGCCCTCCATGACACACCCCTCGATTCTCGACAA	656	
QY	1392	CCAGAGGAGATACRGCTGCTTTAGAAAGAGGGGCACTCTTAGATCCAGGATAGCCCYGTC	1451	
Db	655	CCAGAGGAGATACAGCTGCTTTAGGAAGAGGGGCACTCTTAGATCCAGGATAGCCCGCTC	596	
QY	1452	TGFGGCCAGTGTGGAAGCTGCTCCCATCTCAACTCTCCCTGAGRSCACAGGTGCTGTGAG	1511	
Db	595	TGFTGCCAGTGTGGAAGCTGCTCCCATCTCAACTCTCCCTGAGRSCACAGGTGCTGTGAG	536	
QY	1512	CGCTGTGTCTGCGGGAAAAAGCCGGGGGCTGCATCACACCTCAGAGCTGTTCAGGAAG	1571	
Db	535	GAGCTGTGTCTGCGGGAAAAAGCCGGGGGCTGCATCACACCTCAGAGCTGTTCAGGAAG	476	
QY	1572	CTGCTCTGTCTCAGACAGTCTTCAGTTCCTCTCTGCTCTACACAGAGCCCTTGCTKGG	1631	
Db	475	CTGCTCTGTCTCAGACAGTCTTCAGTTCCTCTCTGCTCTACACAGAGCCCTTGCTGCG	416	
QY	1632	CTGGATGTGGATTCCACCACACAGCCGCTCGCGCACTGTGCCTACAGGTGCTACGCCACC	1691	
Db	415	CTGGATGTGGATTCCACCACACAGCCGCTCGCGCACTGTGCCTACAGGTGCTACGCCACC	356	
QY	1692	TGGCGCTTCGGCTCCCAAGGACATGGCTGATTTTGGCATCTCGGCCAGCTGCTGCCGTGG	1751	
Db	355	TGGCGCTTCGGCTCCCAAGGACATGGCTGATTTTGGCATCTCGGCCAGCTGCTGCCGTGG	296	

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QY 1752 AGATCCGGAAGAGTTTCORAGAGTGNAGGGCAGTACAGTGGCTTCAGAGTCCCTAC 1811
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Db 295 AGATCCGGAAGAGTTTCORAGAGTGNAGGGCAGTACAGTGGCTTCAGAGTCCCTAC 236
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1812 TGAAGCCAGGACCGTGGCTCAGCTGTGTAAATCCCACTTTT 1853
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 235 TGAAGCCAGGACCGTGGCTCAGCTGTGTAAATCCCACTTTT 194
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
BF347290 543 bp mRNA linear EST 22-NOV-2000
LOCUS 602021043P1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156427
5' mRNA sequence.
ACCESSION BF347290
VERSION BF347290.1 GI:11294885
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 543)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA library Preparation: Life Technologies, Inc.
CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9429 row: f column: 12
High quality sequence stop: 543.
FEATURES
source
1. 543
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:4156427"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.3 Kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 148 a 122 c 155 g 118 t
ORIGIN
Query Match 23.28; Score 430; DB 12; Length 543;
Best Local Similarity 98.98; Pred. No. 5.1e-105;
Matches 463; Conservative 1; Mismatches 1; Indels 3; Gaps 3;
QY 5 CGCAGGAGGAGGCTGCACATCGCGGCTGTCGAGCTGCAGTGCAGTATTTTCAGTA 64
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Db 49 CGCAGGAGGAGGCTGCACATCGCGGCTGTCGAGCTGCAGTGCAGTATTTTCAGTA 108
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QY 65 TGAGACGAACAAGTCACTCGGATCCAGATCCAGAGCATGAATATGGCACCATTAAAGTGGTCTT 124
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Db 109 TGAGACGAACAAGTCACTCGGATCCAGATCCAGAGCATGAATATGGCACCATTAAAGTGGTCTT 168
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 125 CCACGTGATCATCTTTTCTACGTTGCTTGTCTGCTGAGTGCACAGCTGACCAGG 184
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Db 169 CCACGTGATCATCTTTTCTACGTTGCTTGTCTGCTGAGTGCACAGCTGACCAGG 227
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QY 185 GAAGAGCCCTGTATCATCTTCTGTGCACACCAAGTGAAGGGGATAGCAGAGTGAAGA 244
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 228 GAAGAGCCCTGTATCATCTTCTGTGCACACCAAGTGAAGGGGATAGCAGAGTGAAGA 287
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QY 245 GGAGATCGTGGAGAAATGAGGTGAAGAAGTGGTGGCACAGTGTCTTTGACACCGCAGACTA 304
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Db 288 GGAGATCGTGGAAATGGAGTGAAGAAGTGGTGGCAGAGTGC-TTGACACCGCAGACTA 346
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QY 305 CACCTTCCCTTTTCAGAGGGAACCTTTTCTTCGTGATGACAAAACCTTTCTCAAAACAGAGG 364
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Db 347 CACCTTCCCT-TTCAGAGGGAACCTTTTCTTCGTGATGACAAAACCTTTCTCAAAACAGAGG 405
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 365 CCAAGAGCAGCGGTTGTGTCCCGAGTATCCCAACCGCAGGAGGCTTCTTCTCTGACCG 424
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 406 CCAAGAGCAGCGGTTGTGTCCCGAGTATCCCAACCGCAGGAGGCTTCTTCTCTGACCG 465
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 425 AGGTTGTAAAAGAGGATGATGAGCCCGCAGAGCAAGGAATTCAGAC 472
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Db 466 AGGTTGTAAAAGAGGATGATGAGCCCGCAGAGCAAGGAATTCAGAC 513
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RESULT 13
BF554327 642 bp mRNA linear EST 20-JUN-2002
LOCUS H4027E01-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
DEFINITION H4027E01 5', mRNA sequence.
ACCESSION BF554327
VERSION BF554327.1 GI:21455215
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 642)
AUTHORS VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin
P.R., Stagg,C.A., Bassey,U., Aliba,K., Hamatani,T., Kargul,G.J.,
Luo,A.G. and Ko,M.S.H.
TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse
cDNA clone set
JOURNAL Unpublished (2002)
COMMENT Other ESTs: H4027E01-3
Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdnaelg@sun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7.4K.html for details.
Seq primer: -21M13 Reverse
High quality sequence stop: 642
POLYA-No.
FEATURES
source
1. 642
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="niaEST:H4027E01-5"
/db_xref="taxon:10090"
/clone_lib="H4027E01"
/clone_lib="NIA Mouse 7.4K cDNA Clone Set"
/sex="mixed"
/lab_host="DH10B"
/notes="Vector: pSPORT1; Site.1: SalI; Site.2: NotI; This
clone is among a rearayed set of 7,407 clones from more
than 20 cDNA libraries."
BASE COUNT 133 a 199 c 179 g 131 t
ORIGIN
Query Match 21.68; Score 399.6; DB 14; Length 642;
Best Local Similarity 80.28; Pred. No. 9.2e-97;
Matches 465; Conservative 3; Mismatches 112; Indels 0; Gaps 0;
QY 1242 GAATCCCATAGTAGTGTGACACGACGCTACTAGGAGAGTCTGCAAGATGTCAG 1301
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Db 1 GAGCGCACATTCGATCGTGGTGGACGACGCTGCTTGGGAAAAGTCTGCAAGTTGCAAA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1302 GGCAGAGAGTCCSAAAGACCTGTGATGACTCACAGATTTGCCAGGCTGCCCTGCC 1361
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Db 61 GGCAGAGAGTTCACAGACCCAGATGGACTTCTCCGACCTGTAGGTGTCCTATCT 120
 QY 1362 CTCCTATGACACCCCGGATCTCTGGACACACAGAGGATACGCTGTAGGAAGGAG 1421
 Db 121 CTCACGACTACCCCTGATCTCTGGACATCTGAGGAATTCAGCTGCTCCATGAGAG 180
 QY 1422 GGGATCTCTAGATCAGGATAGCCCGTCTGTGCTGCCAGTGTGGAGCTGCTCCCATCT 1481
 Db 181 GTGGCCCTTAAGTCGGGGACAGCCGAGTGTGTCAGTGTGGAAATTCCTCCGCTCT 240
 QY 1482 CAACTCTCTGAGGCGACAGCTGCTGGAGGCGCTGTGCTCCGCGAAAGCGGGGGCC 1541
 Db 241 CGCCTACCGGAGCAACGACGCGCCCTGGAGAGCTGTGCTCGCGAGGAAGCGGGGGG 300
 QY 1542 TGCATCACACCTCAGAGCTGTTCAGGAAGCTGTTCCTGCTCCAGACACGCTCCAGCTTC 1601
 Db 301 TGCATCACACCTCAGAGCTGTTCAGGAAGCTGTTCCTGCTCCAGACACGCTCCAGCTTC 360
 QY 1602 CTCCTGCTCTACAGGAGCCCTTGTCTKGCGCTGATGTGATTCACACACAGCGCGCTG 1661
 Db 361 CTCCTGCTTACAGGAGCCCTTGTCTKGCGCTGATGTGATTCACACACAGCGCGCTG 420
 QY 1662 CGGCACTGTGCTACAGTGTGCTAGCCACCTGCGCTGCTGCTCCGAGACATGCTGAC 1721
 Db 421 CGACACCGTGTACAGTGTGCTATGCCACCTGCGCTGCTGCTCCGAGGACATGCCCGAC 480
 QY 1722 TTTGGCATCTGCGCCAGCTGCTGCGCTGAGGATCGGAAAGATTCACAGAGTGAA 1781
 Db 481 TTTGGCATCTGCGCCAGCTGCTGCGCTGAGGATTCGGAAGAGTTTCCCAAGACCGAG 540
 QY 1782 GGGCACTAGTGGCTTCAAGAGTCTCTTACTGAAGCCAGG 1821
 Db 541 GGGCACTAGTGGCTTCAAGATATCCCTACTGATGGTACG 580

RESULT 14

LOCUS BG769470
 DEFINITION 602742429F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4872270 5', mRNA linear EST 15-MAY-2001
 mRNA sequence.
 ACCESSION BG769470
 VERSION BG769470.1 GI:14080123
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cypabs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LCM1748 row: i column: 07
 High quality sequence stop: 555.
 Location/Qualifiers
 1..783
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4872270"
 /clone_lib="NIH_MGC_49"
 /tissue_type="melanotic melanoma, high MDR (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned

FEATURES

source

into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library. |"

BASE COUNT 215 a 206 c 213 g 149 t

ORIGIN

Query Match 21.1%; Score 390.2; DB 12; Length 783;
 Best Local Similarity 94.1%; Pred. No. 3.6e-94;
 Matches 479; Conservative 3; Mismatches 16; Indels 11; Gaps 7;
 QY 5 CGCAGGAGGGAGGCTGTCACCATGCGGCTGCTGCAGCTGCAGTGTCTTCCAGTA 64
 Db 49 CGCAGGAGGGAGGCTGTCACCATGCGGCTGCTGCAGCTGCAGTGTCTTCCAGTA 108
 QY 65 TGAGACGAACAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAAGTGTCTT 124
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 QY 125 CCAGCTGATCATCTTTTCTTACGTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 184
 Db 169 CCAGCTGATCATCTTTTCTTACGTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 228
 QY 185 GAAAGAGCCTGTCATCAGTCTGTCACACCAAGTGAAGGGGATACAGAGTGAAGA 244
 Db 229 GAAAGAGCCTGTCATCAGTCTGTCACACCAAGTGAAGGGGATACAGAGTGAAGA 288
 QY 245 GGAGATCGYGGAGAAATGAGTGTG---AAGAAGTGTGTCACCA--GTGCTCTTTGACACCGCAG 300
 Db 289 GGAGATCGYGGAGAAATGAGTGTG---AAGAAGTGTGTCACCA--GTGCTCTTTGACACCGCAG 348
 QY 301 ACTACACCTTCCCTTTGAGGGGAACTCTTTCTTCTGT---GATGACAAATTTCTCAAAA 357
 Db 349 ACTACACCTTCCCTTTGAGGGGAACTCTTTCTTCTGT---GATGACAAATTTCTCAAAA 408
 QY 358 CAGAAGGCCCAAGAGCAG--CGGTGTGTCGCGAGTATCCACCGC--CAGGACGC--TCTGTT 414
 Db 409 CAGAAGGCCCAAGAGCAGCCGGTGTGTCGCGAGTATCCACCGC--CAGGACGCATCTGAT 468
 QY 415 CCTCTGACCCGAGTTGTAA--AAAGGGATGGATGGACCCCGACAGACAAAGGAATTCAGACC 473
 Db 469 CCTCTGACCCGAGTTGTAA--AAAGGGATGGATGGACCCCGACAGACAAAGGAATTCAGACC 528
 QY 474 GGAAGTGTGTAGTATGATGAGGGAACCA 502
 Db 529 GGAAGTGTGTAGTATGATGAGGGAACCA 557

RESULT 15

LOCUS BF347097
 DEFINITION 602020852F1 NCLCGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156452
 5', mRNA sequence.
 ACCESSION BF347097
 VERSION BF347097.1 GI:11294692
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 555)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cypabs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.

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OM nucleic - nucleic search, using sw model
Run on: July 18, 2003, 15:41:30 ; Search time 4799 Seconds
(without alignments)
11237.237 Million cell updates/sec
Title: US-09-977-221-2
Perfect score: 1853
Sequence: 1 aaacgcaggaggaggtc.....cgtctgtaatccacacattt 1853

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2:	gb_htg.*	
3:	gb_in.*	
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29:	em_vi.*	
30:	em_htg_hum.*	
31:	em_htg_inv.*	
32:	em_htg_other.*	
33:	em_htg_mus.*	
34:	em_htg_pln.*	
35:	em_htg_rdd.*	
36:	em_htg_man.*	
37:	em_htg_vrt.*	
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40:	em_htgo_mus.*	
41:	em_htgo_other.*	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	1846.6	99.7	1853	6	AX427649	AX427649 Sequence
2	1846.6	99.7	1853	9	HSP2X7	Y09561 H.sapiens m
3	1845	99.6	1853	6	AR116693	AR116693 Sequence
4	1837.8	99.2	2164	9	BC011913	BC011913 Homo sapi
5	1836.2	99.1	2168	6	AX099420	AX099420 Sequence
6	1429.2	77.1	2011	9	AK090866	AK090866 Homo sapi
7	1282.4	69.2	3540	6	AR116692	AR116692 Sequence
8	1282.4	69.2	3540	10	TNP2X7GEN	X95882 R.norvegicu
9	1270.8	68.6	1810	10	MMU9823	AJ009823 Mus muscu
10	529.6	28.6	171065	2	AC011216	AC011216 Homo sapi
11	528	28.5	6839	9	HSP2X7123	Y12855 Homo sapien
12	528	28.5	228935	2	AC059209	AC059209 Homo sapi
13	390.2	21.1	504	4	AF083073	AF083073 Bos tauru
14	351	18.9	115282	2	AC130133	AC130133 Rattus no
15	345.6	18.7	66872	2	AC117579	AC117579 Mus muscu
16	345.6	18.7	76175	2	AC115728	AC115728 Mus muscu
17	345.6	18.7	161746	2	AC114632	AC114632 Mus muscu
18	296.2	16.0	364	4	AF005154	AF005154 Bos tauru
19	285.2	15.4	4425	5	XL345114	AJ345114 Xenopus l
20	267	14.4	378	10	AF365362	AF365362 Meriones
21	242	13.1	1765	5	AF020315	AF020315 Gallus ga
22	242	13.1	1803	5	AF218449	AF218449 Gallus ga
23	238.6	12.9	1762	6	BD007172	BD007172 Human p2x
24	237.8	12.8	1189	10	MMU251459	AJ251459 Mus muscu
25	237.8	12.8	1944	10	AF089751	AF089751 Mus muscu
26	237	12.8	1389	9	HSP2X4FC	Y07684 H.sapiens m
27	237	12.8	1762	6	AR026669	AR026669 Sequence
28	236.6	12.8	3090	9	AF191093	AF191093 Homo sapi
29	236.6	12.8	2048	9	HSU83993	U83993 Human p2x4
30	236.2	12.7	1997	10	RNP2X4REC	X87763 R.norvegicu
31	235.4	12.7	1206	6	AR156454	AR156454 Sequence
32	235.4	12.7	1759	6	A65875	A65875 Sequence 1
33	235.4	12.7	1824	9	BC033826	BC033826 Homo sapi
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35	234.6	12.7	1997	6	A47359	A47359 Sequence 6
36	234.6	12.7	1997	6	AR086632	AR086632 Sequence
37	234.6	12.7	1997	6	AR134626	AR134626 Sequence
38	233	12.6	1430	10	RNRNAP2X4	X91200 R.norvegicu
39	231.4	12.5	1917	10	RNU47031	U47031 Rattus norv
40	229.8	12.4	1793	10	RNU32497	U32497 Rattus norv
41	229.2	12.4	1429	5	GGY18008	Y18008 Gallus gall
42	228.8	12.3	1621	9	HSAP000234	AF000234 Homo sapi
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44	226.8	12.2	2129	5	AF308149	AF308149 Xenopus l
45	225.2	12.2	2163	5	AF308151	AF308151 Xenopus l

ALIGNMENTS

RESULT 1	AX427649	1853 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	AX427649	Sequence 2 from Patent EP1199372.			
DEFINITION	AX427649				
ACCESSION	AX427649				
VERSION	AX427649.1	GI:21537769			
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE 1
AUTHORS Morten J.E.
TITLE Polymorphisms in the human p2x7 gene
JOURNAL Patent: EP 1199372-A 2 24-APR-2002;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Db 657 GAACAATATCGACTTCCCGGCGACAACTACACACAGAGAAACATCTGCCAGTTTAAA 716
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Db 717 CATCATCTGTAACCTCCACAGACTCAGAACTCCAGCTGCCATTTTCGGACTAGGAGA 776
QY 725 CATCTTCCGAGAAACAGCGCATATTTTCAGATCGGCAATTCAGGCGGGAATATGGG 784
Db 777 CATCTCCGAGAAACAGCGCATATTTTCAGATCGGCAATTCAGGCGGGAATATGGG 836
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DEFINITION Sequence 60 from Patent WO0119988.
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VERSION AX099420.1 GI:13538536
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 2168)
AUTHORS Jacobs K., McCoy J.M., Lavallie E.R., Collins-Racie L.A., Evans C.,
Merberg D., Treacy M., Bowman M.R., Spaulding V. and Agostino M.J.
TITLE Secreted proteins and polynucleotides encoding them
JOURNAL Patent: WO 0119988-A 60 22-MAR-2001;
Genetics Institute, Inc. (US)
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VERSION AK090866.1 GI:21749107
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REFERENCE 1
AUTHORS Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S.,
Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Watsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Matsumura, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuhara, T., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
TITLE Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 2011)
AUTHORS Isogai, T. and Yamamoto, J.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamata, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp. Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-6F18
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 171065)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
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Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
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Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
JOURNAL Direct Submission
COMMENT Submitted (03-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2000 this sequence version replaced gi:7272137.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WITB
Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu
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Center project name: L2887
Center clone name: 6_F_18
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Chemistry: Dye-terminator Big Dye; 100% of reads
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Insert size: 169065; sum-of-contigs
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Quality coverage: 5.0 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
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* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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 Best Local Similarity 97.4%; Pred. No. 8.7e-124;
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QY 1312 TCCTCAAGACCTGGATGACCTTCACAGATTGTCAGAGCTGCCCTGGCCCTCCATGACA 1371
 |||
 Db 104760 TTCAGAGACCTCGATGACCTTCACAGATTGTCAGAGCTGCCCTGGCCCTCCATGACA 104819
 QY 1372 CACCCCGCATCTCTGGCAACACAGAGAGATACRGCTGTAGAAAGAGGCGACTCCTTA 1431
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 Db 104820 CACCCCGCATCTCTGGCAACACAGAGAGATACAGCTGCTAGAAAGAGGCGACTCCTTA 104879
 QY 1432 GATCCAGGATAGCCCTGCTGTGCGAGTGAGAGCTGCGAGCTGCCCTCCACTCCCTG 1491
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 Db 104880 GATCCAGGATAGCCCTGCTGTGCGAGTGAGAGCTGCGAGCTGCCCTCCACTCCCTG 104939
 QY 1492 AGGCCACAGGTGCTGGAGGAGCTGTGCTGCCGGAAGGCGGGGCTGCATCAACA 1551
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 Db 104940 AGGCCACAGGTGCTGGAGGAGCTGTGCTGCCGGAAGGCGGGGCTGCATCAACA 104999
 QY 1552 CTTAGAGCTGTTCAGAGAGCTGTGCTGCCGGAAGGCGGGGCTGCATCAACA 1611
 Db 105000 CTTAGAGCTGTTCAGAGAGCTGTGCTGCCGGAAGGCGGGGCTGCATCAACA 105059
 QY 1612 ACCAGAGCCCTGCTGCGGTGAGTGTGATTCACCAACAGCGGCTGCGGACATGTG 1671
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 Db 105060 ACCAGAGCCCTGCTGCGGTGAGTGTGATTCACCAACAGCGGCTGCGGACATGTG 105119
 QY 1672 CTTAGAGCTGTTCAGAGAGCTGTGCTGCCGGAAGGCGGGGCTGCATCAACA 1731
 |||
 Db 105120 CTTAGAGCTGTTCAGAGAGCTGTGCTGCCGGAAGGCGGGGCTGCATCAACA 105179
 QY 1732 TGCCCGAGCTGTGCGGTGAGAGTCCGGAAGAGTTCCCAAGAGTGAAGGCGAGTACA 1791
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 Db 105180 TGCCCGAGCTGTGCGGTGAGAGTCCGGAAGAGTTCCCAAGAGTGAAGGCGAGTACA 105239
 QY 1792 GTGGCTTCAAGAGTCTTACTGAGCGAGCGACCGCTGCTCAGCTCTGTAATCCACCTT 1851
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 Db 105240 GTGGCTTCAAGAGTCTTACTGAGCGAGCGACCGCTGCTCAGCTCTGTAATCCACCTT 105299
 QY 1852 TT 1853
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 Db 105300 TT 105301

RESULT 13
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 DEFINITION Bos taurus P2X7 mRNA, partial cds.
 ACCESSION AF083073
 VERSION AF083073.1 GI:5880352
 KEYWORDS
 SOURCE Bos taurus.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 504)
 AUTHORS Smith, R.A. and Estes, D.M.

TITLE Direct Submission
 JOURNAL Submitted (07-AUG-1998) Veterinary Pathobiology, University of Missouri, 201 Conaway Hall, Columbia, MO 65211, USA
 FEATURES
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 TCEVFTWC"

BASE COUNT 138 a 106 c 138 g 122 t
 ORIGIN

Query Match 21.1%; Score 390.2; DB 4; Length 504;
 Best Local Similarity 85.7%; Pred. No. 1e-88;
 Matches 431; Conservative 2; Mismatches 70; Indels 0; Gaps 0;

QY 27 ATGCCGGCTGTGACAGTGCAGTGATGTTTCCAGTATGACAGACAAAGTCTACTGG 86
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 Db 1 ATGCCGGCTGTGACAGTGCAGTGATGTTTCCAGTATGACAGACAAAGTCTACTGG 60
 QY 87 ATCCAGAGCATGAATATGGCACCATTAAAGTGTCTTCCAGTATGATCATCTTTCTTAC 146
 |||
 Db 61 ATCCAGAGCATGAATATGGCACCATTAAAGTGTCTTCCAGTATGATCATCTTTCTTAC 120
 QY 147 GTTTGCTTGGCTGTGAGTGACAAAGTGTACACGGGAAAGAGCCGTGTATCAGTTCT 206
 |||
 Db 121 ATTGGCTTTGCTTGGTGAAGTGAAGTGTATGATGCTCTTCCAGTGTGCTCTTCTTCT 180
 QY 207 GTSCACACCAAGTGAAGGAGTACAGAGTCAAGAGAGATCGYGGAGATGGAGTG 266
 |||
 Db 181 GTSCACACCAAGTGAAGGAGTACAGAGTCAAGAGAGATCGYGGAGATGGAGTG 240
 QY 267 AAGAAGTGTGTCAGAGTGTCTTTGACACCGCAGACTACACCTTCCCTTTGACGGGAAAC 326
 |||
 Db 241 AAGAAGTGTGTCAGAGTGTCTTTGATGATGCGGATACACCTTCCCTTTGACGGGAAAC 300
 QY 327 TCCTTTCTGTCAGTCAAACTTCTCAAAAGAGAGCCAAAGACAGCGCTTGTGTCC 386
 |||
 Db 301 TCCTTTCTGTCAGTCAAACTTCTCAAAAGAGAGCCAAAGACAGCGCTTGTGTCC 360
 QY 387 GAGTATCCACCGCAGAGCTGTCTCTCTGACCGAGGTGTGAAAAGGAGTGATG 446
 |||
 Db 361 GAGTATCCACCGCAGAGCTGTCTCTCTGATCGGGGTGTGAAAAGGAGTGATG 420
 QY 447 GACCCGACAGCAAGGAATTCAGACCGGAGGTGTGTATGATGAGGAGACCAAGAG 506
 |||
 Db 421 GGCCCGGAGCAAGGAATTCAGACCGGAGGTGTGTATGATGAGGAGACCAAGAG 480
 QY 507 ACTGTGAGTCTGCTGCTGTG 529
 |||
 Db 481 ACCTGTGAAGTCTTCACCTGGT 503

RESULT 14
 AC130133/c
 LOCUS AC130133 115282 bp DNA linear HTG 08-AUG-2002
 DEFINITION Rattus norvegicus clone CH230-83K8, *** SEQUENCING IN PROGRESS ***,
 56 unordered pieces.
 ACCESSION AC130133
 VERSION AC130133.1 GI:22138361
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE
AUTHORS

- * This record will be updated with the finished sequence
- * as soon as it is available and the accession number will
- * be preserved.

* This record will be updated with the finished	1	1043: contig of 1043 bp in length
* as soon as it is available and the accession n	1044	1143: gap of unknown length
* be preserved.	1144	2335: contig of 1092 bp in length
	2336	2335: gap of unknown length
	2336	3360: contig of 1025 bp in length
	3361	3460: gap of unknown length
	3461	5110: contig of 1650 bp in length
	5111	5210: gap of unknown length
	5211	6373: contig of 1163 bp in length
	6374	6473: gap of unknown length
	6474	7569: contig of 1096 bp in length
	7570	7669: gap of unknown length
	7670	9379: contig of 1710 bp in length
	9380	9479: gap of unknown length
	9480	10384: contig of 1505 bp in length
	10385	11084: gap of unknown length
	11085	12588: contig of 1504 bp in length
	12589	12688: gap of unknown length
	12689	13994: contig of 1306 bp in length
	13995	14094: gap of unknown length
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	21564	21663: gap of unknown length
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	23073	23372: gap of unknown length
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	29551	30050: gap of unknown length
	30051	32024: contig of 1974 bp in length
	32025	32124: gap of unknown length
	32125	33665: contig of 1741 bp in length
	33666	33965: gap of unknown length
	33966	35946: contig of 1881 bp in length
	35947	35946: gap of unknown length
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	37507	37606: gap of unknown length
	37607	38228: contig of 1322 bp in length
	38229	39028: gap of unknown length
	39029	40222: contig of 1194 bp in length
	40223	40322: gap of unknown length
	40323	42278: contig of 1956 bp in length
	42279	42378: gap of unknown length
	42379	44337: contig of 2059 bp in length
	44338	44537: gap of unknown length
	44538	46448: contig of 1911 bp in length
	46449	46548: gap of unknown length
	46549	47752: contig of 1204 bp in length
	47753	47852: gap of unknown length
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	50099	51493: contig of 1394 bp in length
	51494	51593: gap of unknown length
	51594	53443: contig of 1850 bp in length
	53444	53543: gap of unknown length
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Rattus.

1 (bases 1 to 115282)

Muzny,D.M., Adams,J.C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrook,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,C., Blankenbiller,K., Bonnin,D., Bouck,J., Bowie,S., Brleva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrge,N.C., Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J.J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davilla,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Dellaney,K.R., Delgado,O., Dennon,A.L., Ding,Y., Dinth,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earhart,C., Edgar,B., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.J., Foster,P., Frantz,P., Gabis,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlik,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsif,P., Howard,S., Huber,J.J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,O., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N.C., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lien,C., Liu,J., Liu,W., Loulsegad,H., Lozados,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Pace,A., Payton,B., Peery,J., Perez,L., Massey,E., Mawlinye,F., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragune,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rivers,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabar,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usman,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 115282)

Worley,K.C.

Direct Submission

Submitted (08-Aug-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

----- Genome Center -----

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information -----

Center project name: GHYX

Center clone name: CH230-83R8

----- Summary Statistics -----

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 56769 bases at least Q40

Consensus quality: 59422 bases at least Q30

Consensus quality: 61794 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

TITLE JOURNAL REFERENCES AUTHORS TITLE JOURNAL	COMMENT
<p>1. TITLE JOURNAL REFERENCES AUTHORS TITLE JOURNAL</p>	

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* 97142 99951: contig of 2810 bp in length
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* 107841 107940: gap of unknown length
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Matches 405; Conservative 4; Mismatches 94; Indels 0; Gaps 0;
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DB 105345 CACCCCAATCTCTGGACAACTGAGGAATGACAGTGTCTCCAGATAGAGGGTTCCTA 105286
QY 1432 GATCCAGGATAGCCCTGCTGTGGTCCAGTGTGAAGCTGCCCTCCATCTCAATCCCTG 1491
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QY 1552 COTCAGAGCTGTTCCAGAGAGTGGCTGTCTCCAGACAGCTGCTGAGTCTCTGCTCT 1611
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DB 104985 TGCCAGCTGCTGCCGCTGGAGATCCGGAAGAGTTCCTCCAGACCCAGGGGCGACTACA 104926
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ACCESSION AC117579
VERSION AC117579.2 GI:20976671
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 66872)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Mus musculus, clone RP23-37P22
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 66872)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
Bookhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Gaigani,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Larocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mlenka,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,N., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 66872)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
Bookhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Larocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
Meneus,L., Mihova,T., Mlenka,V., Murphy,T., Naylor,J., Nguyen,C.,
Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
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Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigglio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE JOURNAL

Submitted (18-Mar-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 18, 2002 this sequence version replaced g1:20128322.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L22320

Center clone name: 37_P_22

*** NOTE: This record contains 85 individual
*** sequencing reads that have not been assembled into
*** contigs. Runs of N are used to separate the reads
*** and the order in which they appear is completely
*** arbitrary. Low-pass sequence sampling is useful for
*** identifying clones that may be gene-rich and allows
*** overlap relationships among clones to be deduced.
*** However, it should not be assumed that this clone
*** will be sequenced to completion. In the event that
*** the record is updated, the accession number will
*** be preserved.

1
685 784: contig of 684 bp in length
785 1487: contig of 703 bp in length
1488 1587: gap of 100 bp
1588 2264: contig of 677 bp in length
2265 2364: gap of 100 bp
2365 3042: contig of 678 bp in length
3043 3142: gap of 100 bp
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3813 3912: gap of 100 bp
3913 4598: contig of 686 bp in length
4599 4698: gap of 100 bp
4699 5388: contig of 690 bp in length
5389 5488: gap of 100 bp
5489 6175: contig of 687 bp in length
6176 6275: gap of 100 bp
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6967 7066: gap of 100 bp
7067 7758: contig of 692 bp in length
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12468 12567: gap of 100 bp
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14843 14942: gap of 100 bp
14943 15631: contig of 689 bp in length
15632 15731: gap of 100 bp
15732 16424: contig of 693 bp in length
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* 16525 17209: contig of 685 bp in length
* 17210 17309: gap of 100 bp
* 17310 18011: contig of 702 bp in length
* 18012 18111: gap of 100 bp
* 18112 18809: contig of 698 bp in length
* 18810 18909: gap of 100 bp
* 18910 19588: contig of 679 bp in length
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Query Match 18.7%; Score 345.6; DB 2; Length 66872;
Best Local Similarity 79.4%; Pred. No. 3.8e-77;
Matches 405; Conservative 3; Mismatches 102; Indels 0; Gaps 0;

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QY 1432 GATCCAGGATAGCCCTCTCGGTGCCAGTGTGGAAAGCTGCCCTCCCATCTCAACTCCCTG 1491
Db 38142 AGTCCGGGACAGCCCGAGTTGGTCCAGTGTGAAATTCCTCCCTCTCGCTACCGG 38201
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QY 1552 CCTCAGAGCTGTTCAGGAAGTGGTCTCTGTCCAGACAGCTCTGCAGTTCTCTCTGTCT 1611
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QY 1612 ACCAGGAGCCCTTGTCTGCGGTGGATGTGATTCACCAACAGCCGGGTGCGGCACTGTG 1671
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Job time : 4814 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 15:40:30 ; Search time 444 Seconds
(without alignments)
9398.543 Million cell updates/sec

Title: US-09-977-221-2

Perfect score: 1853

Sequence: 1 aaacgcaggaggagggct.....cgtctgtaatccacacctttt 1853

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1846.6	99.7	1853	24	AA143027 Human P2X7 gene co
2	1845	99.6	1853	22	AAC63694 Human P2X7/P22 co
3	1836.2	99.1	2168	22	AAF98411 Human cDNA clone C
4	1833.4	98.9	2169	19	AAV30932 Human secreted pro
5	1282.4	69.2	3540	22	AAC63693 Rat P2X7/P22 codi
6	237	12.8	1762	19	AAV27197 HPUR nucleic acid
7	235.4	12.7	1206	22	AAH25211 Nucleotide sequenc
8	235.4	12.7	1759	18	AAV09307 Human brain P2X-1
9	234.6	12.7	1997	17	AAT33853 Rat superior cervi

10	233.8	12.6	1207	22	AA04979 Human purinergic r
11	227.2	12.3	1807	18	AAV09308 Human brain P2X-2
12	203.8	11.0	2833	24	ABK84338 Human cDNA differe
13	203.8	11.0	2833	24	ABK84338 Pancreas cancer re
14	203.8	11.0	2643	17	AAT33855 Human urinary blad
15	196.4	10.6	294	20	AAV89619 EST clone CO390.
16	168.8	9.1	1784	23	AAST6004 DNA encoding novel
17	159.6	8.6	1837	17	AAT33852 Rat vas deferens p
18	148.4	8.0	1272	20	AAV87357 Human P2X3 puriner
19	148.4	8.0	1272	21	AAC64099 Human P2X-3 recept
20	148.4	8.0	1272	22	AAC64096 Human P2X3 cDNA 5'
21	148	8.0	1243	20	AAV87356 Human P2X3 puriner
22	148	8.0	1243	21	AAC64101 Human P2X-3 recept
23	148	8.0	1243	22	AA04966 Human purinergic r
24	147.4	8.0	4900	24	AA143026 Human P2X7 gene 5'
25	145.8	7.9	1272	22	AA04988 Human P2X3 cDNA 5'
26	142.6	7.7	11366	24	AA143028 Human P2X7 gene in
27	140.2	7.6	1753	17	AAT33854 Rat dorsal root ga
28	140	7.6	1421	21	AAZ51322 Human purino recep
29	140	7.6	1421	22	AAH25208 Nucleotide sequenc
30	140	7.6	1436	21	AAZ51321 Human purino recep
31	140	7.6	1436	22	AAH25207 Nucleotide sequenc
32	138.6	7.5	1240	22	AA04982 Human purinergic r
33	138.4	7.5	1349	21	AAZ51323 Human purino recep
34	138.4	7.5	1349	22	AAH25209 Nucleotide sequenc
35	138.2	7.5	1639	23	ABK43717 DNA encoding novel
36	135.6	7.3	1499	21	AAZ51324 Human purino recep
37	135.6	7.3	1499	22	AAH25210 Nucleotide sequenc
38	111.6	6.0	564	22	AAI92047 Human polynucleoti
39	111	6.0	1697	19	AAV61833 Coding sequence fo
40	109.4	5.9	1293	19	AAV61832 Coding sequence fo
41	107.8	5.8	1360	22	AA04978 Human purinergic r
42	102.6	5.5	1856	24	ABK09794 Human ovarian tumo
43	102.6	5.5	1986	24	ABK84338 Human cDNA differe
44	101.2	5.5	1973	24	ABN59853 Novel human coding
45	96.8	5.2	878	15	AAQ73761 RP-2 Programmed ce

ALIGNMENTS

RESULT 1

AA143027 AAL43027 standard; DNA; 1853 BP.

XX AC AAL43027;

XX DT 08-AUG-2002 (first entry)

XX DE Human P2X7 gene coding sequence.

XX KW Human; ds; single nucleotide polymorphism; SNP; P2X7-associated disorder;
KW inflammation; immune disease; drug development; genetic marker; gene;
KW P2X7 gene.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 27..1814

FT FT /*tag= a

FT FT /product= "Human P2X7 protein"

FT FT replace (253, C)

FT FT /*tag= b

FT FT /note= "Single nucleotide polymorphism"

FT FT replace (488, A)

FT FT /*tag= c

FT FT /note= "Single nucleotide polymorphism"

FT FT replace (489, T)

FT FT /*tag= d

FT FT /note= "Single nucleotide polymorphism"

FT FT replace (760, G)

FT FT /*tag= e

FT FT /note= "Single nucleotide polymorphism"

[illegible]

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Db	481	GTGTAGTATGAGGGAAACACAGAACCTGTGAAGTCTGTGCTGGTCCGCCCATCGAGG	540	Db	1561	TGTTCCAGAACCTGGTCTGTCCAGACAGCTCCCTGCAGTTCCTCTCTACACAGGAGC	1620
QY	541	CAGTGAAGAGAGCCCGCCCTGCTCTTGAACAGTGCAGAAACTTCACGTGCTCA	600	QY	1621	CCTTCTXGCGCTGGATGTGGATTCACCAACAGCCGGCTGGCGCACTGTGCTACAGGT	1680
Db	541	CAGTGAAGAGAGCCCGCCCTGCTCTTGAACAGTGCAGAAACTTCACGTGCTCA	600	Db	1621	CCTTCTGCGCTGGATGTGGATTCACCAACAGCCGGCTGGCGCACTGTGCTACAGGT	1680
QY	601	TCAAGAACAAATATGCACTTCCCGGGCCACAACTACACACAGAGAACTCCCTGCCAGTT	660	QY	1681	GCTAGCCACCTGGCGCTTCCAGGACATGGCTGACTTTGCCATCTCTGCCAGCT	1740
Db	601	TCAAGAACAAATATGCACTTCCCGGGCCACAACTACACACAGAGAACTCCCTGCCAGTT	660	Db	1681	GCTAGCCACCTGGCGCTTCCAGGACATGGCTGACTTTGCCATCTCTGCCAGCT	1740
QY	661	TAAACATCACTGTGTAATTCACAACTCAGATTCACAGTGTCCGATTTTCGAGTAG	720	QY	1741	GCTGCGCTGGAGATCCGGAAGAGTTTCCGAAGAGTGTAGGGCAGTACAGTGCTTCA	1800
Db	661	TAAACATCACTGTGTAATTCACAACTCAGATTCACAGTGTCCGATTTTCGAGTAG	720	Db	1741	GCTGCGCTGGAGATCCGGAAGAGTTTCCGAAGAGTGTAGGGCAGTACAGTGCTTCA	1800
QY	721	GAGACATCTCCGAGAACAGGGGATAATTTTCAGATGKGCATTTTCAGGCGGAATAA	780	QY	1801	AGAGTCTTACTGAAAGCAGGACCGTGGCTCAGCTCTGTAAATCCCACTTTT	1853
Db	721	GAGACATCTCCGAGAACAGGGGATAATTTTCAGATGKGCATTTTCAGGCGGAATAA	780	Db	1801	AGAGTCTTACTGAAAGCAGGACCGTGGCTCAGCTCTGTAAATCCCACTTTT	1853
QY	781	TGGGCATTTGATGATGAGTGTGGAATGCAACTAGACCGTGTGCTTCCATCACTGCCATCA	840	RESULT 3			
Db	781	TGGGCATTTGATGATGAGTGTGGAATGCAACTAGACCGTGTGCTTCCATCACTGCCATCA	840	AAF98411			
QY	841	AATACAGTTTCCTGCGCTTACAGACAGACACCAACCGTGTCTTGTACCTTGGCTACA	900	ID	AAF98411 standard; cDNA; 2168 BP.		
Db	841	AATACAGTTTCCTGCGCTTACAGACAGACACCAACCGTGTCTTGTACCTTGGCTACA	900	XX	AC AAF98411;		
QY	901	ACTTCAGATACCCAACTACTACAAGGAAACAAATGTTGAGAACGGACTCTGATAAAG	960	XX	07-JUN-2001 (first entry)		
Db	901	ACTTCAGATACCCAACTACTACAAGGAAACAAATGTTGAGAACGGACTCTGATAAAG	960	XX	Human cDNA clone CO390_1 sequence SEQ ID 60.		
QY	961	TCTTGGGATCGTTTTCATCTGCTGTTTGGACCGGAGGAAATTTGACATATACC	1020	XX	Human; secreted protein; nutrient; cytokine modulator; proliferation;		
Db	961	TCTTGGGATCGTTTTCATCTGCTGTTTGGACCGGAGGAAATTTGACATATACC	1020	KW	differentiation; immune system modulator; tissue growth; chemotactic;		
QY	1021	AGCTGTTGTGATGATCGCTCAACCTCTCTACTTCTGGCTGGCCCTGTGTTCTATCG	1080	KW	haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;		
Db	1021	AGCTGTTGTGATGATCGCTCAACCTCTCTACTTCTGGCTGGCCCTGTGTTCTATCG	1080	XX	Homo sapiens.		
QY	1081	ACTTCTCATGACACTTACCAAGTAACTGTCTGCTCCCTCAATATTTATCCCTGTGCA	1140	XX	WO200119988-A1.		
Db	1081	ACTTCTCATGACACTTACCAAGTAACTGTCTGCTCCCTCAATATTTATCCCTGTGCA	1140	XX	22-MAR-2001.		
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Db	1141	AGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1200	XX	17-SEP-1999; 99US-0398829.		
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Db	1201	TGGAGCCAAAGCCGACATTAAGTATGATGATGATGATGATGATGATGATGATGATG	1260	PI	Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;		
QY	1261	TGAACACAGCTACTAGGAGAGTCTCAAGATGTCACAGGCGCAAGAGTCCSAGAC	1320	PI	Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;		
Db	1261	TGAACACAGCTACTAGGAGAGTCTCAAGATGTCACAGGCGCAAGAGTCCSAGAC	1320	XX	WPI; 2001-244801/25.		
QY	1321	CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1380	DR	P-PSDB; AAB90689.		
Db	1321	CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1380	XX	Isolated nucleic acids encoding polypeptides, useful for modulating		
QY	1381	TTCTTGGACACACAGAGAGATACAGCTGTGAGAGAGGCGGACTCTAGATCCAGGG	1440	PT	e.g. cytokine and cell proliferation/differentiation activity, the		
Db	1381	TTCTTGGACACACAGAGAGATACAGCTGTGAGAGAGGCGGACTCTAGATCCAGGG	1440	PT	immune system and hematopoiesis regulating activity -		
QY	1441	ATAGCCCTGTGTCAGTGTGAGAGTGTGTCCTCCATCTCACTCCCTGTAGAGCCACA	1500	PS	Disclosure; Page 419; 557pp; English.		
Db	1441	ATAGCCCTGTGTCAGTGTGAGAGTGTGTCCTCCATCTCACTCCCTGTAGAGCCACA	1500	CC	Human cDNA clones represented in AAF98374 - AAF98489 encode secreted		
QY	1501	GGTGCTGAGAGGCTGTGTCGCGGAAAGCCGGCGCTGCATCACCACCTCAGAGC	1560	CC	proteins AAB90667 - AAB90750. The cDNA clones are isolated from various		
Db	1501	GGTGCTGAGAGGCTGTGTCGCGGAAAGCCGGCGCTGCATCACCACCTCAGAGC	1560	CC	tissue types, and may be used in the prevention, treatment and diagnosis		
				CC	of diseases associated with inappropriate protein expression. The		
				CC	polypeptides and nucleic acids may be used as nutrients or to modulate		
				CC	cytokine and cell proliferation/differentiation activity and may also be		
				CC	involved in modulation of the immune system. The cDNA sequences,		
				CC	proteins, their agonists and/or antagonists exhibit haematopoiesis		
				CC	regulating activity; tissue growth activity; activin/inhibin activity;		
				CC	chemotactic/chemokinetic activity; haemostatic and thrombolytic		
				CC	activity; receptor/ligand activity; anti-inflammatory activity;		
				CC	haematopoiesis activity; cadherin/tumour suppressor activity; and/or		
				CC	tumour inhibition activity. Included in the invention are probes		

CC represented in AAF98490 - AAF98572 which are specific for the cDNA clones
CC encoding the secreted proteins.

XX Sequence 2168 BP; 539 A; 583 C; 577 G; 469 T; 0 other;

Query Match 99.1%; Score 1836.2; DB 22; Length 2168;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1829; Conservative 16; Mismatches 4; Indels 0; Gaps 0;

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Db 65 CGAGGGAGGAGGTGTCACCATGCGCGGCTGCTGCAGCTGCAGTGCAGTGTTCACGTA 124
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   |||
Db 125 TGAGAGCAACAAGTCACTCGGATCCAGAGCATGAATTATGSCACCAATTAAGTGGTCTT 184
   |||
QY 125 CCAGTGTATCATCTTTTCCACGTTTGGCTTGTCTGCTGAGTGACAAAGCTGTACCAGCG 184
   |||
Db 185 CCAGTGTATCATCTTTTCCACGTTTGGCTTGTCTGCTGAGTGACAAAGCTGTACCAGCG 244
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RESULT 4

AAV30932

ID AAV30932 standard; DNA; 2169 BP.

XX AC AAV30932;

XX AC AAV30932;

XX DT 14-SEP-1998 (first entry)

XX DE Human secreted protein C0390_1 cDNA.

XX KW C0390_1; secreted protein; protein factor; human; ds.

XX

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QY 1025 GGTGTGTACATCGGCTCAACCCCTCTCTACTTCTGCTGCGCCCTGTGTTCATCGACTT 1084
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Db 1085 GGTGTGTACATCGGCTCAACCCCTCTCTACTTCTGCTGCGCCCTGTGTTCATCGACTT 1144
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QY 1085 CTTATCTGACATCTACTCCAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1144
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   |||
Db 1265 GCCAAAGCCGACATTAAGTATGTCTCTTGTGATGAATCCCAACATTAGGATGTTGAA 1324
   |||
QY 1265 CAGAGAGCTACTAGGAGAACTCTGCAAGATGTCAGAGGCCCAAGATCCCAAGACCTGT 1324
   |||
Db 1325 CAGAGAGCTACTAGGAGAACTCTGCAAGATGTCAGAGGCCCAAGATCCCAAGACCTGT 1384
   |||
QY 1325 GATGGACTTTCACAGATTTGTCAGGCTGCGCCCTGCGCCCTGCGCCCTGCGCCCTGCGCCCT 1384
   |||
Db 1385 GATGGACTTTCACAGATTTGTCAGGCTGCGCCCTGCGCCCTGCGCCCTGCGCCCTGCGCCCT 1444
   |||
QY 1385 TGGACAACAGAGGAGATACRGCTGTGTTAGAAAGGAGGCGACTCCTAGATCCAGGGATAG 1444
   |||
Db 1445 TGGACAACAGAGGAGATACRGCTGTGTTAGAAAGGAGGCGACTCCTAGATCCAGGGATAG 1504
   |||
QY 1445 CCCCTGCTGGTCCGAGTGTGAAGCTCCCTCCCATCTCACTCCCTGAGGCCACAGGTG 1504
   |||
Db 1505 CCCCTGCTGGTCCGAGTGTGAAGCTCCCTCCCATCTCACTCCCTGAGGCCACAGGTG 1564
   |||
QY 1505 CTTGGAGGAGCTGTGCTGCCGGAAGAGCCGCGGCGCTGCATCACCCTCAGAGCTGTT 1564
   |||
Db 1565 CTTGGAGGAGCTGTGCTGCCGGAAGAGCCGCGGCGCTGCATCACCCTCAGAGCTGTT 1624
   |||
QY 1565 CAGGAAGCTGCTCTGTCTCCAGACACGCTCTGCAAGTTCCTCTGCTCTTACCAGAGCCCTT 1624
   |||
Db 1625 CAGGAAGCTGCTCTGTCTCCAGACACGCTCTGCAAGTTCCTCTGCTCTTACCAGAGCCCTT 1684
   |||
QY 1625 CTTGCGCTGGAATGGAATCCACCAACAGCCGCGCTGCGGCACTGCGCTACAGGTGCTA 1684
   |||
Db 1685 CTTGCGCTGGAATGGAATCCACCAACAGCCGCGCTGCGGCACTGCGCTACAGGTGCTA 1744
   |||
QY 1685 CGCCACTGCGCTTCTGCTCCAGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1744
   |||
Db 1745 CGCCACTGCGCTTCTGCTCCAGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1804
   |||
QY 1745 CCGCTGAGGATCCCGGAAGAGTTCCTCAAGAGTGAAGGCGCAGTACAGTGGCTTCAAGAG 1804
   |||
Db 1805 CCGCTGAGGATCCCGGAAGAGTTCCTCAAGAGTGAAGGCGCAGTACAGTGGCTTCAAGAG 1864
   |||
QY 1805 TCCCTACTGAAGCCAGGCAACCGTGGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1864
   |||
Db 1865 TCCCTACTGAAGCCAGGCGCGTGGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1913
   |||
```

RESULT 4

AAV30932

ID AAV30932 standard; DNA; 2169 BP.

XX AC AAV30932;

XX AC AAV30932;

XX DT 14-SEP-1998 (first entry)

XX DE Human secreted protein C0390_1 cDNA.

XX KW C0390_1; secreted protein; protein factor; human; ds.

XX

[illegible]

Db 1385 GATGGATTACAGATTGTCCAGGCTGCCCTGGCCCTCCATGACACACCCCGATCC 1444
QY 1385 TGGACACAGAGGAGATACGCTGCTTAGAAGAGGGGAGCTCTATGATCCAGGATAG 1444
Db 1445 TGGACACAGAGGAGATACGCTGCTTAGAAGAGGGGAGCTCTATGATCCAGGATAG 1504
QY 1445 CCYGTGCTGGTGGCTGGAAGCTGCTCCCATCTCAACTCCCTGAGGCCACAGGTG 1504
Db 1505 CCCGCTGGTGGCTGGAAGCTGCTCCCATCTCAACTCCCTGAGGCCACAGGTG 1564
QY 1505 CTTGAGGAGCTGCTGCTGGGAGAAAGCCGGGGGCTGCTATCACCACCTCAGAGCTGTT 1564
Db 1565 CTTGAGGAGCTGCTGCTGGGAGAAAGCCGGGGGCTGCTATCACCACCTCAGAGCTGTT 1624
QY 1565 CAGGAAGCTGCTGCTGCTGACACAGCTGCTGAGTCTCTCTCTACAGGAGCCCTT 1624
Db 1625 CAGGAAGCTGCTGCTGCTGACACAGCTGCTGAGTCTCTCTCTACAGGAGCCCTT 1684
QY 1625 GCTGCGCTGGATGGATTCACCAACAGCGGGCTGCGGCACTGCTACAGGTGCTA 1684
Db 1685 GCTGCGCTGGATGGATTCACCAACAGCGGGCTGCGGCACTGCTACAGGTGCTA 1744
QY 1685 CGCCACCTGGCGCTTGGCTGCCAGGACATGGCTGACTTGGCATCTCTGCCAGCTGCTG 1744
Db 1745 CGCCACCTGGCGCTTGGCTGCCAGGACATGGCTGACTTGGCATCTCTGCCAGCTGCTG 1804
QY 1745 CCCTGAGGATCCGGAAGAGTTTCCCAAGAGTGAAGGCGAGTACAGTGGCTTCAAGAG 1804
Db 1805 CCCTGAGGATCCGGAAGAGTTTCCCAAGAGTGAAGGCGAGTACAGTGGCTTCAAGAG 1864
QY 1805 TCCTTACTGAAGCCAGGACCGCTGGCTCAAGTCTGTAATCCCACTTTT 1853
Db 1865 TCCTTACTGAAGCCAGGACCGCTGGCTCAAGTCTGTAATCCCACTTTT 1913

RESULT 5
AAC63693
ID AAC63693 standard; cDNA; 3540 BP.
AC AAC63693;
XX
DT 13-FEB-2001 (first entry)
XX Rat P2X₇/P2Z coding sequence.
DE
XX Rat; P2X₇; neuroprotective; nootropic; antiinflammatory; antirheumatic;
KW antiarthritic; antibacterial; antiviral; antiallergic; cyostatic;
KW cardiant; cerebroprotective; immunosuppressive; P2₇; purinergic receptor;
KW nervous system disorder; chronic inflammation; Alzheimer's disease;
KW rheumatoid arthritis; amyloidosis; bacterial; viral; microbial infection;
KW haematopoietic system disorder; immune response; autoimmune disorder;
KW allergy; lymphoproliferative disorder; cardiac; cerebral ischaemia;
KW tuberculosis; ss.
XX
OS Rattus sp.
XX
XX US6133434-A.
XX
PD 17-OCT-2000.
XX
XX 28-APR-1997; 97US-0842079.
XX
PR 28-APR-1997; 97US-0842079.
XX (GLAX) GLAXO GROUP LTD.
XX Buell GN, Kawashima E, Surprenant A;
XX WPI; 2001-006153/01.
DR P-PSDB; AAB28243.
XX
XX Mammalian purinergic receptor (P2X₇) useful for screening for

PT modulators which are useful for treating arthritic, respiratory
PT disorders and neurodegenerative disorders, and to generate receptors
PT specific antibodies -
XX
PS Claim 3; Fig 1B; 40pp; English.
XX
CC The present sequence is the coding sequence for rat purinergic receptor
CC P2X₇/P2Z. This sequence can be used to treat disorders of the nervous
CC system, particularly diseases with a component of chronic inflammation,
CC such as Alzheimer's disease, diseases involving acute or chronic
CC inflammation such as rheumatoid arthritis, amyloidosis, bacterial, viral
CC and other microbial infections, disorders of the haematopoietic system
CC and immune response such as autoimmune disorders, allergies and
CC lymphoproliferative disorders, diseases involving apoptotic cell death,
CC such as cardiac and cerebral ischaemia and microbial infections,
CC particularly tuberculosis.
XX
SQ Sequence 3540 BP; 919 A; 958 C; 899 G; 764 T; 0 other;
Query Match 69.2%; Score 1282.4; DB 22; Length 3540;
Best Local Similarity 81.4%; Pred. No. 0;
Matches 1469; Conservative 12; Mismatches 323; Indels 0; Gaps 0;
QY 11 GAGGAGGAGCTGTCCACCATCCGCGCTGCTGCAGCTGCAGTGTGTTTCCAGTATGAGAC 70
Db 106 GAGTGAGCCTGTGCCATCGCGCTTGTGCTGAGCTGGAAGATGCTTTCAGTATGAGAC 165
QY 71 GAACAAGTCACTCGGATCCAGAGCATGAATATGAGCACCATTAAAGTGTGTTTCCAGCT 130
Db 166 AAACAAGTCACTCGGATCCAGAGCATGAATATGAGCACCATTAAAGTGTGTTTCCAGCT 225
QY 131 GATCATCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190
Db 226 GACGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 285
QY 191 GCTGCTCATCAGTCTGTGTCCACACCAAGGTGAAGGGATAGCAGAGGTGAAGAGAGAT 250
Db 286 GCGCTTATCAGCTGTGTCCACACCAAGGTGAAGGGATAGCAGAGGTGAAGAGATGT 345
QY 251 GYGAGAGATGGAGTGAAGATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 310
Db 346 CACGAGGGGGGTGTGAGAGT 405
QY 311 CCCTTTCAGGGAGTCTTTCTGCTGATGACAAATTTCTCAAGTCAGAGGCGCAGA 370
Db 406 CCCTTTCAGGGAGTCTTTCTGCTGATGACAAATTTCTCAAGTCAGAGGCGCAGA 465
QY 371 GCAGCGGTGTGTCCGAGTATCCACCGCAGGACGCTGTCTCTCTGACGAGGTG 430
Db 466 ACAGAAGCTGT 525
QY 431 TAAAGAGATGGATGGATCCGAGAGCAAGAGTTCAGACGGAAGTGTGTGTGTGTGTGTGT 490
Db 526 TATAAAGATGGATGGATCCGAGAGCAAGAGTTCAGACGCGGAGGTGTGTGTGTGTGTGT 585
QY 491 TGAAGGAGACCAAGACCTGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
Db 586 CGACCCAGAGAGAGAGACCTGTGAAATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
QY 551 GCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610
Db 646 AGCCCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
QY 611 TATGAGTTCGCGGCGCAACTACACAGAGAAATCTGCGAGGTGTGTGTGTGTGTGTGTGTGT 670
Db 706 TATGAGTTCGCGGCGCAACTACACAGAGAAATCTGCGAGGTGTGTGTGTGTGTGTGTGTGT 765
QY 671 TTGTACCTTCCACAGACTCAGAAATCCAGTGTCCCATTTTCCGAGTAGAGACATCTT 730
Db 766 TTGTACCTTCCACAGACTTGGAACTTCCGAGTAGAGACATCTT 825
QY 731 CGAGAGAACAGGCGATAATTTTTCAGATGKGCATTTTCAGGCGGGAATAATGCGCATTTGA 790

Db 182 AGGCTACCAAGAACTGACTCCGTGGTCACTCCGTAGACCAAGGTCAAGGGCTGG 241
QY 232 CAGAGGTGAAGAGGAGATCGYGGAGATGGAGTGAAGTGGTGCACAGTCTCTTG 291
Db 242 CTGTGACCAACACTTCAACATGGATTCGGGATCGGGATTCGGGATTCATGTATG 301
QY 292 ACACCGCAGACTACACTTCCTTTGAGGGGAACCTTTCTGCTGATGACAAATTC 351
Db 302 CAG-----CTCAGGAGAAACTCCCTCTGCTGATGACCAACTGA 343
QY 352 TCRAAACAAGAGCCAGAGAGCGGTGTCTCCGAGTATCCACCCGAGGAGCTCT 411
Db 344 TCCACCATCAACACAGACAGAGGCTGTGCCCGAGATCCAGATCGACCACTGTGT 403
QY 412 GTTCTCTGACCGAGTGTGAAGAGGATGATGACCGGAGAGCAAGAAATTCAGA 471
Db 404 GTAATCAGATGCCAGCTGTACTGCCGGCTCTGCCGACCCACACAGCAACGATCA 463
QY 472 CCGAAGGTGTGTATGATGAAGGAGACAGAGACCTGTGAAGTCTCTGCTGTGGCC 531
Db 464 CAGCAGGTGCTGAGCTTTCACGGGTCCGTCAAGAGCTGTGAGGTGGCGCTGGTGC 523
QY 532 CCATCGAGGAGTGAAGAGGCGCCCGGCTGTCTGTGAACAGTCCCGAAACTCA 591
Db 524 CGGTGGAGATGACACACAGCTGTGCCAACAACCTTTTAAAGGCTGCAGAACTCA 593
QY 592 CTGTGCTCATCAGACATATFCGACTTCCCGGCGCACAACTACACACGAGAAATCC 651
Db 584 CTCCTTTGGTGAAGAACATCTGTGTATCCCAATTTAATTTACAGAGAGGAATCC 643
QY 652 TGCAGGTTTAAATCACT-----TGTACTTCCACAGACTCAGAAATCCAC 699
Db 644 TTCCACATACACACTACTTACCTCAAGTCGTGATATGATGCTAAACAGATCCCT 703
QY 700 AGTGTCCATTTCCGACTAGAGACATFTCCGAGAAACAGCGCATATTTTCAGATG 759
Db 704 TCTGCCCATATTCCTCTTGGCAAAATAGTGGAGAACGACGACACAGTTCCAGACA 763
QY 760 KGGCAATTCAGGCGGAATATGAGCAATGAGATCTGAGTCTGAGCTGCAACCTAGACGTT 819
Db 764 TGGCCGTGGAGGAGGAGCATCATGGCAATCCAGCTCAACTGGGACTGCAACCTGGACAG 823
QY 820 GTTTCATCACTCCCTCCCAATACAGTTTCCTGTGCTGTGACGACAGACCCACAG 879
Db 824 CCGCTCCCTCTCTGCTGCCAGGACTCTTCCGCGCCCTCGATACAGGAGCTTGAGC 883
QY 880 TGTCTTGTACCTGCTACAACTTCAGATACGCCAAGTACTACAGGAAACAAATG--- 936
Db 884 ACAAGTATCTCTGCTACAACTTCAGGTTTGGCAAGTACTACAGAGACCTGGCTGCA 943
QY 937 TTGAGAAACGACTCTGTATAAGTCTTCGGGATCCGTTTGACATCTGTTTGGCA 996
Db 944 ACAGAGAGCCAGCGTCATCAAGGCTATGGCATCCGCTTCGACATCTTGTGTTGGA 1003
QY 997 CGGAGGAAATTTGACATATTCAGCTGTGTGTGATACATCGGCTCAACCTCTCTACT 1056
Db 1004 AGGAGGAAATTTGACATATTCAGCTCAACCTCAATGATCAACATCGGCTCTGGCACTGC 1063
QY 1057 TCGTCTGGCCCTGTGTTTCATCGACTTTCCTCATC 1091
Db 1064 TAGCATGGGACCGTGTGTGATCATATGATC 1098

RESULT 7

AAH25211

ID AAH25211 standard; DNA; 1206 BP.

XX AC

XX AAH25211;

XX AC

DT 22-AUG-2001 (first entry)

XX AC

Nucleotide sequence of a human purinoreceptor P2X4.

Human; purinoreceptor; P2X2; P2X4; pain; neuroendocrine disease;
auditory disease; vestibular disorder; ss.
Homo sapiens.
Key Location/Qualifiers
CDS 21..1187
FT /*tag= a
FT /product= "purinoreceptor P2X4"

US6242216-B1.

05-JUN-2001.

13-NOV-1998; 98US-0191608.

14-NOV-1997; 97US-0065822.

20-AUG-1998; 98US-0137458.

(ABBO) ABBOTT LAB.

Lynch KJ, Burgard EC, Metzger RE, Niforatos W, Touma EB;

Van Biesen T;

WPI; 2001-388837/41.

P-PSDB; AAB84382.

Isolated polynucleotides, used to produce P2X2 receptor polypeptides and
identify potentially therapeutic compounds, encode a human P2X2
receptor polypeptide -
Example 4; Fig 11; 40pp; English.

The specification describes nucleic acids encoding a functional human
purinoreceptor polypeptides P2X2 and P2X4. P2X polypeptides and
polynucleotides are used to identify modulators, which may be used to
treat and prevent pain, diseases of the neuroendocrine system, and
auditory and vestibular disorders. P2X and P2X polynucleotides are a
source of probes and primers, which may be used to identify homologous
sequences, for gene localisation studies, and for gene therapy purposes.
The polynucleotides may also be used to produce the polypeptide
recombinantly. The P2X polypeptides are used to arise antibodies, and
to identify inhibitors. The present sequence encodes human P2X4.

Sequence 1206 BP; 285 A; 335 C; 320 G; 266 T; 0 other;

Query Match 12.7%; Score 235.4; DB 22; Length 1206;

Best Local Similarity 54.3%; Pred. No. 3.5e-54;

Matches 573; Conservative 5; Mismatches 441; Indels 36; Gaps 4;

QY 55 TTTTCCAGTATGAGACGACAAAGTCACTCGATCCAGACATGAAATATGACCACTTA 114

Db 55 TTTTCCAGTATGAGACGACGCGCATCGTCTCATCCGACGCGCAAGTGGGCTCATGA 114

QY 115 AGTGTCTTCCAGGTGATCATCTTTTCTCTAG--TTTCTTTTCTGTTGAGTGACA 171

Db 115 ACCGCGCGGTGCACT 174

QY 172 AGCTGTACACGCGAAGAGCGCTGTCTATCATCTGTGTGACACCAAGGTGAAGGGGATAG 231

Db 175 AGGGCTACCGAAGTACTGCTCGTGGTCACTCGTTCAGACCAAGGTGAAGGGGATAG 234

QY 232 CAGAGGTGAAGAGGAGATCGTGGAGATGAGAGTGAAGAGTGGTGGACAGTGTCTTTG 291

Db 235 CTGTGACCAACACTTCTAAACTTGGATTCCGGATCTGGGATGTGGGATTTATGTATC 294

QY 292 ACACCGCAGACTACACTTCCCTTTTCAGAGGAGACTTTTCTCTGATGACAACTTC 351

Db 295 CAG-----CTCAGAGGAGAAACTCCCTCTTCGTCATGACCAAGTGA 336

QY 352 TCRAAACAAGAGCCAGAGAGCGGTGTGCTCCGAGATATCCACCCGAGGAGCTCT 411

Db 337 TCTTCACCATGACCAAGAGAGAGGCGCTGTGCCCGAGATTCAGATGCGACCATGTGT 396

```
QY 412 GTTCCTCTCACCAGGTTGTAAAGAGGATGATGACCCGACAGCAAGAAATTCAGA 471
DB 397 GTAATCAGATGCCAGCTGTACATGCGGCTCTGCGGACCCACAGCAAGAGTCTCAA 456
QY 472 CCGGAAGTGTGTAGTATGAAGGGAACAGAGACCTGTGAAGTCTCTGCTGGTCC 531
DB 457 CAGGAGGTGCTAGCTTCAACGGTCCGTCAGAGCTGTGAGTGGGGCTGTGTC 516
QY 532 CATGAGGAGTGAAGAGGCCCCCGGCTGTCTCTGACAGTGGCGGAACTTCA 591
DB 517 CGGTGAGGATGACACACAGCTGTCACAACTCTCTTTTAAAGGCTGCGAGAACTTCA 576
QY 592 CTGTGCTCATCAAGAACAAATAGTCTCCCGGCGCACACTACACACAGAGAAATCC 651
DB 577 CTCCTTTGTTAAGACACATCTGTATCCCAATTAATTCAGCAGAGGATATCC 636
QY 652 TGCAGGTTTAAACATCACT-----TGTAACCTTCCCAAGACTCAGAATCCAC 699
DB 637 TTCCCAACATCACCCTACTTACCTCAAGTCTGCTGATTTATGCTTAAACAGATCCCT 696
QY 700 AGTGTCCATTTCCGCTAGGAGACATCTCCGAGAAACAGGCGATATTTTCAGATG 759
DB 697 TGTGCCCATATTCGCTTGGCAAAATAGTGAGAACGCGAGGACGGTTTCCAGGACA 756
QY 760 KGCATATTCAGGCGGGAATAGGCAATGAGATCTACTGGCACTGCAACCTAGACCGTT 819
DB 757 TGGCGGTGAGGAGGATCATGGGATCCAGTCACTGGACTGCACTGCACTGGACAG 816
QY 820 GGTTCATATCTGCGCTCCCAATACATGTTCCCTTCGCTTTCAGCAAGACCAACG 879
DB 817 CGCGCTCCCTCTGCTTCCAGGTACTCTCTCCGCGGCTCGATACACAGGACGTTGAGC 876
QY 880 TGTCTTGTACCTGGCTACAACTTCAGTACGCGACGACTACTACAGGAAACATG--- 936
DB 877 ACAAGTATCTCTGGCTACAAATTCAGGTTTCCCAAGTACTACAGAGACCTGGCTGCA 936
QY 937 TTGAGAAACGACTCTGATAAAGTCTTCGGATCCGTTTTCATCTGGTTTGGCA 996
DB 937 ACAGCAGCGACGCTCATCAGCGCTATGCGATCCGTTGCACTATGTTGGGA 996
QY 997 CCGGAGGAAATTTGACATATCCAGCTGGTTGTGTATACGCTGCTCAACCTCTCTACT 1056
DB 997 AGCAGGGAATTTGACATATCCCACTATGATCAACATCGGTCTGCGCTGGCAGCTGC 1056
QY 1057 TCGGCTGCGCCTGTGTTTCATCGACTTCTCTATC 1091
DB 1057 TAGGATGCGACCGTGTGTGTGATCATATGTC 1091
```

RESULT 8

```
AAV09307
ID AAV09307 standard; cDNA; 1759 BP.
XX
AC AAV09307;
XX
DT 18-MAY-1998 (first entry)
XX
DE Human brain P2X-1 receptor encoding cDNA.
XX
KW Brain; P2x receptor; treatment; trauma; spinal cord; infection;
KW human; inflammation; mood disorder; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT a
FT /product= "Human brain P2X-1 receptor"
XX
PN W09741222-1.
XX
PD 06-NOV-1997.
```

```
XX 30-APR-1996; 96WO-GB01034.
PF
XX 30-APR-1996; 96WO-GB01034.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA (SMIK ) SMITHLINE BEECHAM PLC.
XX
PI Carpenter DJ, Livingstone CD, McHALE MT, Tomlinson WJ;
PI Y1 L;
XX
XX WPI; 1997-549726/50.
XX P-PSDB; AAW47066.
XX
XX DNA encoding human brain P2x receptors - used to develop products
XX for treating, e.g. brain or spinal cord traumas, infection,
XX inflammation and mood disorders
XX
XX Claim 6; Fig 1; 31pp; English.
XX
XX This cDNA encodes a human brain P2X-1 receptor polypeptide. The P2X
XX receptor splice variants (P2X-1, P2X-2 and P2X-3 isoforms) can be
XX recombinantly expressed by a host cell genetically engineered with a
XX vector containing the encoding nucleic acids. The receptors can be used
XX to screen for their antagonists. The products can be used to identify
XX agents which modulate the activity of the receptors for use in clinical
XX conditions such as brain stroke, brain or spinal cord traumas, infection
XX and inflammation, cognitive disorders, epilepsy, affective and mood
XX disorders in general, including depression, various movement disorders
XX including Parkinson's disease, Huntingtons Chorea and schizophrenia, as
XX well as those conditions that are associated with the development of
XX chronic or acute forms of pain, or cardiac anoxia. The products can also
XX be used for detection, production of antibodies and production of
XX transgenic animals as models for mutation and structure/activity
XX relationship evaluations as well as in drug screening.
XX
XX Sequence 1759 BP; 402 A; 496 C; 480 G; 381 T; 0 other;
XX
XX Query Match 12.78; Score 235.4; DB 18; Length 1759;
XX Best Local Similarity 54.38; Pred. No. 4.2e-54;
XX Matches 573; Conservative 5; Mismatches 441; Indels 36; Gaps 4;
XX
QY 55 TTTTTCAGTATGAGACGAAACAAATGCTCGGATCCGATCAGAGCATGAATATGGCACCATTA 114
DB 48 TGTTCAGTATGAGACGACCCCGCGCATGCTCTCATCCGACGCCGCAAGTGGGGCTCATCA 107
QY 115 AGTGGTTTCCACGTGATCATCTTTTCCTAG---TTTGGCTTTGCTCTGGTGAATGACA 171
DB 108 ACCGGCGGTGCAACTGCTCATCTCTGCTCTAGCTCATCGGCTGGGTGTTTGTGGGAAA 167
QY 172 AGCTGTACCAGGGAAGAGCCTGTATCATGTTCTGTGCACACCAAGTCAAGGGATAG 231
DB 168 AGGGCTACCCAGGAAACACTGCTCGGTGGTCTCGGTACGACCAAGGTCAAGGGCTGG 227
QY 232 CAGAGTGAAAGAGGAGATCGYGGAGAAATGGAGTGAAGAGTTGGTGCACAGTGTCTTTG 291
DB 228 CTGTGACCAACACTCTTAACATTGGATTCCGGATCCGGATGTGGCGGATATGTGATAC 287
QY 292 ACACGCCAGCTACACCTTCCCTTTTCAGGGAACTCTTTCTCGTGATGACAAACTTTC 351
DB 288 CAG-----CTCAGGAGGAAAACTCCCTCTTCGTCATGACCAAGTGA 329
QY 352 TCAGAACAGAGGCGCAGGAGGTTGTGTCGCGAGTATCCACCCGACAGAGCTCT 411
DB 330 TCTCATCATGAACACAGACACAGCGGCTGTGCCCGAGATTCAGATGCGGACCTGTGT 389
QY 412 GTTCTCTGACCGAGTTGTAAAAAGGGATGGATGGACCCGACAGCAAGAAATTCAGA 471
DB 390 GTAATCAGATGCCAGCTGTACTGCGGCTCTGCGGCGCACCCACAGCAGAGTCTCAA 449
QY 472 CCGGAAGTGTGTAGTATGAAGGGAACAGAGACCTGTGAAGTCTCTGCTGGTCC 531
DB 450 CAGGCGGTGCTAGCTTTCACGGGTCTGTCAAGACGTGTGAGTGGGGCTGTGTC 509
```

QY 532 CCATCGAGCAGTGGAGAGGCCGCCCGGCGCTGCTCTTGAACAGTGCACAACTTCA 591
 Db 510 CGGTGGAGGTGACACACACGTCGCCACAACTGCTTTTAAAGGCTGCAGAAACTTCA 569
 QY 552 CTGTGCTCATCAAGACAAATATCGACTTCCCGGCCACAACTACACACGAGAAACATCC 651
 Db 570 CTCCTTTGGTTAAGAACACATCTGGTATCCCAATTTAATTTACAGAGAGGATATCC 629
 QY 652 TGCAGGTTTAAACATCACT-----TGTACCTTCCACAGAGACTCAGAAATCCAC 699
 Db 630 TTCCCAACATCACACACTACTTACCTCAAGTCTGTCATTTATGATGCTAAACACAGATCCCT 689
 QY 700 AGTGTCCATTTTCCGACTAGGAGACATCTTCCGAGAAACAGCGCATTTTTCACATG 759
 Db 690 TCTGCCCATATTCCTCTTGGCAAAATAGTGAGAACGCGAGACACAGTTTCCAGGACA 749
 QY 760 KGGCAANTCAGGCGGAATAATAGGCAATGAGATCTACTGGGACTGCACACTAGACCGTT 819
 Db 750 TGGCGGTGGAGGAGCATCATGGCATCCAGTCACTGGGACTGCAACTGGACAGAG 809
 QY 820 GTTCCATCACTGCTCTCCCAATACAGTTTCCCTGCTTGAAGCAAGACACCAACG 879
 Db 810 CCGCTCTCTCTGCTTCCAGGTACTCTTCCCGCGCTCGATACACGGGACCTTGAGC 869
 QY 880 TGTCTGTACCTGCTTCAACTTACATAGTACGCAAGTACTACAGGAACAAATG--- 936
 Db 870 ACAACGATCTCTGCTCAATTTAGGTTTGGCAAGTACTACAGACCTGCTGGCA 929
 QY 937 TTGAAACGGAACCTCTGATAAAGTCTTCCGGATCCGTTTTCACATCTGTTTGGCA 996
 Db 930 ACAGACGCGACGCTCATCAGGCTATGCGATCGCTTCGACATCAITGTGTTGGGA 989
 QY 997 CGGAGGAAATTTGACATATCCAGCTGGTGTGTATACATCGGCTTCAACCTTCCTACT 1056
 Db 990 AGGAGGGAATTTGACATCATCCCACTACATGATCAACATCGGCTCTGGCTGGCACTGC 1049
 QY 1057 TCGTCTGGCCCTGTGTTTCATCGACTTCTCTCATC 1091
 Db 1050 TAGGCATGGGACCGGTGTGTGACATCATGATC 1084

RESULT 9
 AAT33853
 ID AAT33853 standard; cDNA; 1997 BP.
 XX AC AAT33853;
 XX DT 23-NOV-1996 (first entry)
 XX DE Rat superior cervical ganglion P2x receptor cDNA clone 3.
 XX KW ATP P2x receptor; purinoceptor; ligand-gated ion channel; agonist;
 KW antagonist; epilepsy; cognition; emesis; pain; asthma;
 KW peripheral vascular disease; hypertension; irritable bowel syndrome;
 KW premature ejaculation; cystitis; therapy; ss.
 XX OS Rattus sp.
 XX Key Location/Qualifiers
 FT 101..1267
 FT CDS /*tag= a
 FT FT
 XX W09533048-A2.
 XX 07-DEC-1995.
 XX 24-MAY-1995; 95WO-EP01968.
 XX 09-FEB-1995; 95GB-0002480.
 XX 27-MAY-1994; 94GB-0010664.
 XX (GLAX) GLAXO GROUP LTD.

XX Buell GN, Valera S;
 XX WPI; 1996-030561/03.
 XX P-PSDB; AAW04216.
 XX DNA encoding ATP P2x receptors of the purinoceptor family - for
 screening cpds. useful in treating epilepsy, cognition, emesis,
 pain, asthma, peripheral vascular disease, hypertension, etc.
 XX Claim 1; Fig 2; 82pp; English.
 XX Rat P2x clone 3 (AAT33853) codes for the superior cervical ganglion
 CC P2x receptor (AAW04216), a ligand-gated ion channel that opens upon
 CC binding of extracellular ATP. It was isolated by screening a rat
 CC testis cDNA bank with a probe obtd. by PCR amplification of testis
 CC cDNA using primers (see also AAT33857-58, based on the rat vas
 CC deferens P2x receptor cDNA (AAT33852). A rat dorsal ganglion P2x
 CC receptor cDNA (AAT33854) was similarly isolated, and a human homologue
 CC (AAT33855) was also identified. The cDNA can be used to produce
 CC recombinant P2x receptors in host (e.g. COS) cells.
 XX SQ Sequence 1997 BP; 470 A; 523 C; 542 G; 462 T; 0 other;
 Query Match 12.7%; Score 234.6; DB 17; Length 1997;
 Best Local Similarity 55.5%; Pred. No. 7.4e-54;
 Matches 585; Conservative 5; Mismatches 429; Indels 36; Gaps 6;
 QY 55 TTTTCCAGTATGAGACGAAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCAATTA 114
 Db 135 TCTTCGAGTACGACACGCGCGCATCTGTCATCCGACCCGTAAGTGGGGCTCATGA 194
 QY 115 AGTGTCTTCCACGATGATCTTTTCCATAG---TTTGTCTTGTCTGTTGAGTGAACA 171
 Db 195 ACCGCGGGTGCAGCTCTCATCTCGGCTTACGTATCGGGTGGTGTCTGTGGGAAA 254
 QY 172 AGCTGTACCGGCGGAAAGAGCTGTCTCATCTGTGACACCAAGGAGGAGGATAG 231
 Db 255 AGGGCTACGAGAAACGGACTCCGTTGGTCACTCGGTGACCAACCAAGCAAGGTGG 314
 QY 232 CAGAGGTGAAGAGGAGATCGYGGAGAAATGGAGTGAAGAAGTTGGTGACAGTGTCTTTG 291
 Db 315 CTGTGACCAC-----ACCTCTCAGCTTGGATTCGGATCTGGGACGTGGCGGACTATG 368
 QY 292 ACACGCGAGACTACACTTCCCTTTTCGAGGGGAACTCTTTCTTCGTGATGACAACTTTC 351
 Db 369 TGATTTCCAG-----CTCAGAGGAGAAACTCCCTCTTATTATGACCAACATGA 416
 QY 352 TCACAAACAGAGGCGCAGAGCAGCGGTTGTGTCCGAGTATCCACCCGACAGCGCTCT 411
 Db 417 TTGTCCAGCTGACACGACAGACAGACACTGTCCAGAGATCTCTGATAGACACAGCATTT 476
 QY 412 GTTCTCTGACCGAGGTGTGTAAGAGGATGGATGGACCCGACAGACCAAGGAATTCAGA 471
 Db 477 GTAATTCAGACGCGGACTGCTCTCTGCTCCGTTGGACACCCACACAGTGGAGTTGGA 536
 QY 472 CCGGAAGGTGTGTAGTATGAAAGGAAACAGACCTGTGAAGTCTCTGCTCTGGTGGCC 531
 Db 537 CTGGAAGATGTGTTCTTCTTCAATGAGTCTGTGAAGAGCTGTGAGTGGTGTGATGGTGC 596
 QY 532 CCATCGAGGAGTGAAGAGGCGCCCGGCTCTCTCTTGAACAGTGCAGAACTTCA 591
 Db 597 CGGTGGAGACAGCTGTGGCGTGGCAACGCGGCTTTCTTTAAAGGCTGCAGAACTTCA 656
 QY 592 CTGTGCTCATCAAGAACTATCGACTTCCCGGCCCAACTACACGACAGAAACATCC 651
 Db 657 CCTCTTGTGAAGACACACATCTGTATCCCAAGTTTACTTTCACAGAGAGACATCC 716
 QY 652 TGCCAGGTTTAA-----ACATCACTTGTACTTTCCACAAAGACTCA---GAATCCAC 699
 Db 717 TCCCAACATCACACGCTCTCTCAATCGTCAATTTTACATGCTCAACGATCCCT 776
 QY 700 AGTGTCCCATTTTCCGACTAGGAGACATCTTCGAGAAACAGCGGATATTTTTCAGATG 759

```

Db      777  TCTGCCCATATTCGCTTGGCACAATCGTGGGGACGGGACATAGCTCCAGGAGA 836
QY      760  KGGCAATTCAGGCGGAATATGAGCATCTAGATCTACTGGGACTGCACCTAGACCTTT 819
Db      837  TGGCAGTTGAGGAGGAGCATCATGGGTATCCAGATCAAGTGGGACTGCAACCTGGATAG 896
QY      820  GGTCCATCACTGCTCCCAATACAGTTTCCTTCGCTTGACAGCAAGACCAACG 879
Db      897  CGGCTCCCTTGCTGCCAGATATTCCTCCGGCGCTGGACACCGGGACCTGGAC 956
QY      880  TGTCTTTGACCTGGCTAGCAATTCAGATAGCCAGTACTACAAGAA---AACAATG 936
Db      957  ACAATGTGTCTCTGGCTACAAATTCAGGTTCAGGTTCAGAGGACCTGGCGGCA 1016
QY      937  TTGAGAAAGGACATCATAAAGTCTTCGGATCCGTTTGACATCTGGTTTGGCA 996
Db      1017  AAGACAGGACACTCACCAGGCTAGGCATCCGCTTTGACATCTGGTGTGGAA 1076
QY      997  CCGGAGGAAATTTGACATTAATCCAGCTGGTTGTGTATCATCGGCTCAACCTCTCTACT 1056
Db      1077  AGGCTGGGAAGTTTGACATCATCCCTACCATGATCAAGTTGGCTCTGGCTGGCGCTCC 1136
QY      1057  TGGGCTGGGCRCTGTGTTTCATGAGCTTCCTCCTC 1091
Db      1137  TCGGGGTGGCAGGCTGCTCTGTGAGCTCATAGTC 1171

RESULT 10
RAD04979
ID   RAD04979 standard; DNA: 1207 BP.
AC   RAD04979;
DT   17-JUL-2001 (first entry)
DE   Human purinergic receptor P2X4 receptor DNA.
KW   Human; purinergic receptor; P2X4; antidepressant; vulnerary; hypotensive;
KW   anticonvulsant; antiinflammatory; therapy; nervous system disorder;
KW   epilepsy; pain; depression; neurodegenerative disorder; cystic fibrosis;
KW   irritable bowel disorder; reproductive system disorder; hypertension;
KW   peripheral vascular disease; immune system disorder; chronic bronchitis;
KW   premature ejaculation; asthma; neuromuscular disease; ds.
OS   Homo sapiens.
FH   Key
FT   CDS
FT   Location/Qualifiers
FT   21..1186
FT   /*tag= a
FT   /product= "Human P2X4 receptor"
FT   263
FT   misc_feature
FT   /*tag= b
FT   /note= "Represented in the specification as F"
FT
FT
USG214581-B1.
PN
XX
PD   10-APR-2001.
XX
PF   13-NOV-1998; 98US-0191136.
XX
PR   16-JAN-1998; 98US-0071298.
PR   16-JAN-1998; 98US-0071669.
PR   16-JAN-1998; 98US-0008185.
PR   16-JAN-1998; 98US-0008526.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Lynch KJ, Burgard EC, Van Biesen T;
XX
DR   WPI; 2001-315459/33.
XX
PT   Novel isolated polynucleotide encoding human purinergic P2X3 receptor

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PT      polyptide useful for identifying potentially therapeutic compounds
PT      that modulate or otherwise interact with P2X containing receptors
XX
XX      Example 11; Fig 10; 53pp; English.
XX
XX      The present sequence is human P2X4 receptor DNA containing its open
XX      reading frame with EcoRI restriction used for subcloning. P2X
XX      receptors are ligand-gated ion channels while P2Y receptors operate
XX      generally through a G-protein coupled system. P2X purinoreceptor drugs
XX      are potential therapeutic agents in several disorders including central
XX      nervous system or peripheral nervous system conditions, e.g., epilepsy,
XX      pain, depression, neurodegenerative disorders, disorders of the skeletal
XX      muscle such as neuromuscular diseases, disorders of the reproductive
XX      system, asthma, peripheral vascular disease, hypertension, immune system
XX      disorders, irritable bowel disorder, premature ejaculation, cystic
XX      fibrosis and chronic bronchitis. P2Y purinoreceptors mediate the activity
XX      of extracellular nucleotide triphosphates to regulate chloride secretion
XX      in human airway epithelia.

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SQ Sequence 1207 BP; 285 A; 335 C; 320 G; 266 T; 1 other;

```

Query Match      12.68; Score 233.8; DB 22; Length 1207;
Best Local Similarity 54.9%; Pred. No. 9.5e-54;
Matches 581; Conservative 4; Mismatches 432; Indels 41; Gaps 5;

QY      55  TTTTCCAGTATGACAGCAACAAGTCACCTCGGATCCAGACAGATGAATATGCAACCAATTA 114
Db      55  TGTTCGATAGACACGCGCCGCGCATCGTCTCATCCGACGCCCAAGTGGGGCTCAGA 114
QY      115  AGTGTCTTCCACGATGATCACTTTTCTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 171
Db      115  ACCGCGCGCTGCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 174
QY      172  AGCTGTACAGCGGAAGACCTGTCTCATCAGTCTGTGTGACACCAAGGTGAGGGGATAG 231
Db      175  AGGGCTACCGGAAACTGACTCCGTGGTCCAGTCCGTTACGACCAAGGTCAAGGCGGTGG 234
QY      232  CAGAGGTGAAGAGAGAGATCGYGGAGAATGGAGTGAAGAAGTGGTGCACAGTGTCTTTG 291
Db      235  CNGTGACCAAC-----ACITCTAAGCTTGGATTCCCGATCTGGG 274
QY      292  ACACGCGAGCTACACCTTCC---CTTTGAGGGGAACTCTTTCTGCGTATGACAAACT 348
Db      275  ATGTGCGGATATGTATACAGCTCAGAGGAGGAAAACTCCCTCTCTGTCATGACCAACG 334
QY      349  TTCTCAAAACAGAGCGGACAGACGCGGTGTCTCCGAGATATCCACCCCGAGGCGC 408
Db      335  TGATCTCACCATGACACAGACAGGCGCTGTGCCCGGAGATTCCAGATGCGGACCACTG 394
QY      409  TCTGTCTCTCTGACCGAGTTGTAAAAAGGATGGATGGACCGCGCAGACGAAAGAAATTC 468
Db      395  TGTGTAAATCAGATGCCAGCTGTACTGCGGCTCTGCGGCGCACCCACACGAGAGTCT 454
QY      469  AGACCGGAAGTGTGTAGTATGAGGAGACCAAGACCTGTGAAGTCTCTGCTGCTGCT 528
Db      455  CAACAGGCGGTTGTGTGTTCATCAAGGCTCCGTCAGAGGCTGTGAGGTGGCGGCTGCT 514
QY      529  GCCCATCGAGGAGTGGAGAGGCGCCCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 588
Db      515  GCCCGTGGAGATGACACACAGCTGCCCAACTGCTTTTTTAAAGGCTCAGAAAACT 574
QY      589  TCACTGTGCTCATCAGAACAAATATCGACTTCCCGGCGCAACTACACAGCAAGAAACA 648
Db      575  TCACCTCTTTTGGTTAAGACACATCTGTTATCCCAATTAATTTTACAGAGAGGATA 634
QY      649  TCCTGCCAGTTTAAACATCACT-----TGTACCTTCCACAGACTCAGATC 696
Db      635  TCCTTCCCAACATCACCCTACTTACTTACCTCAAGTGTGCTATTTATGATGCTAAACAGATC 694
QY      697  CACAGTGTCCCATTTTCCGACTAGGACATCTTCCGAGAAACAGCGGATATATTTTCAG 756
Db      695  CCTCTGCCCATATTCCTCTTGGCAAAATAGTGGAGAACGAGGACGAGGCTTTTCAGG 754

```


RESULT 13	
ABL70017	
ID	ABL70017 standard; DNA; 2633 BP.
XX	
XX	ABL70017;
XX	
XX	15-MAY-2002 (first entry)
XX	
XX	Pancreas cancer related gene sequence SEQ ID NO:8354.
DE	
DE	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
DE	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytostatic; gene therapy; antineoplastic; wilm's tumour; adenocarcinoma;
KW	gene; ds.
XX	
XX	Homo sapiens.
OS	
XX	WO2001194629-A2.
PN	
XX	13-DEC-2001.
PD	
XX	30-MAY-2001; 2001WO-US10838.
XX	
XX	05-JUN-2000; 2000US-209473P.
PR	
PR	05-JUN-2000; 2000US-209531P.
PR	18-SEP-2000; 2000US-233133P.
PR	18-SEP-2000; 2000US-233617P.
PR	20-SEP-2000; 2000US-234009P.
PR	20-SEP-2000; 2000US-234034P.
PR	20-SEP-2000; 2000US-234052P.
PR	22-SEP-2000; 2000US-234509P.
PR	22-SEP-2000; 2000US-234567P.
PR	25-SEP-2000; 2000US-234923P.
PR	25-SEP-2000; 2000US-234924P.
PR	25-SEP-2000; 2000US-235077P.
PR	25-SEP-2000; 2000US-235082P.
PR	25-SEP-2000; 2000US-235134P.
PR	25-SEP-2000; 2000US-235280P.
PR	26-SEP-2000; 2000US-235637P.
PR	26-SEP-2000; 2000US-235638P.
PR	27-SEP-2000; 2000US-235711P.
PR	27-SEP-2000; 2000US-235720P.
PR	27-SEP-2000; 2000US-235840P.
PR	27-SEP-2000; 2000US-235863P.
PR	28-SEP-2000; 2000US-236028P.
PR	28-SEP-2000; 2000US-236032P.
PR	28-SEP-2000; 2000US-236033P.
PR	28-SEP-2000; 2000US-236034P.
PR	28-SEP-2000; 2000US-236109P.
PR	28-SEP-2000; 2000US-236111P.
PR	29-SEP-2000; 2000US-236842P.
PR	29-SEP-2000; 2000US-236891P.
PR	02-OCT-2000; 2000US-237172P.
PR	02-OCT-2000; 2000US-237173P.
PR	02-OCT-2000; 2000US-237278P.
PR	02-OCT-2000; 2000US-237294P.
PR	02-OCT-2000; 2000US-237295P.
PR	02-OCT-2000; 2000US-237316P.
PR	03-OCT-2000; 2000US-237425P.
PR	03-OCT-2000; 2000US-237598P.
PR	03-OCT-2000; 2000US-237604P.
PR	03-OCT-2000; 2000US-237606P.
PR	03-OCT-2000; 2000US-237608P.
PR	01-NOV-2000; 2000US-244867P.
PR	01-NOV-2000; 2000US-245084P.
XX	
XX	(AVAL-) AVALON PHARM.
XX	
XX	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI	Soppet DR, Weaver Z;
XX	
XX	WPI; 2002-188264/24.


```

Db 1046 A-----ATCTCTCCAGGCTTCAACTTCAGTTTGCAGGCTTTCAGGCTTGTGGAGAC 1096
QY 933 AATGTTGAGAAAGGACTCTGATAAAGTCTTCGGGATCCGTTTGTGACATCTGTTT 992
Db 1097 GGACCACTACCGTCACTCTTCAAGGTTTGGGATTCGCTTTGACATCTTGGTGAC 1156
QY 993 GGCACGGGAGGAGAAATTTGACATATCCAGCTGGTTGTGTACATPCGCTCAACCCCTCTCC 1052
Db 1157 GGCAGGGCGGGAAGTTTGACATCATCCCTACAATGACCACCATPCGCTCGATTTGGC 1216
QY 1053 TACTTCGGTCTGGCCCTGTGTTCAATCGACTTCCT 1087
Db 1217 ATCTTTGGGTGGCCACAGTTCTCTGTGACCTGCT 1251

RESULT 14
ID AAT33855 standard; cDNA; 2643 BP.
XX
AC AAT33855;
XX
DT 23-NOV-1996 (first entry)
XX
DE Human urinary bladder P2x receptor cDNA.
XX
KW ATP P2x receptor; purinoceptor; ligand-gated ion channel; agonist;
KW antagonist; epilepsy; cognition; emesis; pain; asthma;
KW peripheral vascular disease; hypertension; irritable bowel syndrome;
KW premature ejaculation; cystitis; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key
FT Location/Qualifiers
FT 174..1373
FT CDS /tag= a
FT
FT
FT
PN W09533048-A2.
XX
XX 07-DEC-1995.
XX
XX 24-MAY-1995; 95WO-EP01968.
XX
XX 09-FEB-1995; 95GB-0002480.
XX
XX 27-MAY-1994; 94GB-0010664.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Buell GN, Valera S;
XX
XX WPI; 1996-030561/03.
XX
XX P-ESDB; AAW04218.
XX
XX
XX DNA encoding ATP P2x receptors of the purinoceptor family - for
XX screening cpds. useful in treating epilepsy, cognition, emesis,
XX pain, asthma, peripheral vascular disease, hypertension, etc.
XX
XX Claim 1; Fig 4; 82pp; English.
XX
XX A cDNA clone (AAT33855) codes for the human urinary bladder P2x
XX receptor (AAW04218), a ligand-gated ion channel that opens upon
XX binding of extracellular ATP. It was isolated from a bladder
XX cDNA library using a rat smooth muscle P2x receptor probe.
XX Rat vas deferens, superior cervical ganglion and dorsal root
XX ganglion P2x receptor cDNAs (AAT33852-54) have also been isolated.
XX These cDNAs can be used to produce recombinant P2x receptors in
XX host, esp. mammalian, cells for use in screening (ant)agonist
XX cpds.
XX
XX Sequence 2643 BP; 607 A; 794 C; 701 G; 541 T; 0 other;
XX
XX Query Match 11.0%; Score 203.8; DB 17; Length 2643;
XX Best Local Similarity 54.8%; Pred. No. 2.5e-45;
XX Matches 447; Conservative 5; Mismatches 342; Indels 21; Gaps 2;

```

```

QY 285 GTCTTTGACACCGCAGACTACACTTTCCTCTTGAGGGGAACCTCTTCTTCGTGATGACA 344
Db 423 GTCTGGGATGTGGCTGACTACGTCCTTCCAGCCCGAGGGGACAACTCTCTTCGTGTGATG 482
QY 345 AACTTTCTCAAAACAGAGAGCCCAAGAGCAGACGGTTGTCTCCCGAGTATCCCAACCCGACGG 404
Db 483 ACCAATTTTCATCGTGACCCCGAAGCAGAGACTCAAGGCTACTGCGCAGAGCACCCAGAAAGG 542
QY 405 AGCTCTGTCTCTGACCCAGGTTGTAATAAGGGATGGATGGACCCCGCAGAGCAAGAGGA 464
Db 543 GGCATATGCAAGGAGACAGTGTGCTTACCCCTGGGAGGCCAAGAGGAGGCCCAAGGCC 602
QY 465 ATTACAGACCGGAAGTGTGTAGTATGAAGGGAACAGAGACCTGTGAAGTCTCTCC 524
Db 603 ATCCGACGGCAAGTGTGTGGCTTCAACGACACTGTGAAGACGTGTGAGATCTTTGGC 662
QY 525 TGGTCCCCCATCGAGGCAAGAGAGGCCGCCCGGCTGTCTCTTTGAACAGTCCCGAA 584
Db 663 TGGTCCCCGTGGAGGTGGATGACGACATCCCGCGCCCTGCCCTTCTCCGAGAGGCCGAG 722
QY 585 AACTTCACGTGCTCATCAAGAAACATATFCGACTTCCCGGCCACACACTACACACGAGA 644
Db 723 AACTTCACGTCTTTTCATCAAGAAACAGCATCAGCTTTCACGCTTCAAGGTCACAGGGCC 782
QY 645 AACATCCTCCAGAGTTTTAAA-----CATCACTTGTACTTCCACAGACTCAG 692
Db 783 AACCTGGTGGAGGAGTGAATGCTGCCACATGAAGACTCGCTCTTTCACAGACCTTG 842
QY 693 AATCCACAGTGTCCCATTTCCGACTAGAGACATCTTCGAGAAACAGGCGATTAATTTT 752
Db 843 CACCCCTGTGCCAGTCTTCCAGCTTGGCTAGCTGCTGCAAGAGTCAGGCCAGCAATTC 902
QY 753 TCAGATGKGCATTCAGGGGGAATAATGGCANTGAGATCTACTGGGACTGCAACCTA 812
Db 903 AGCACCTGGCTGAGAGGGGTGGAGTGTGTCATCACCATCGACTGGCAGCTGTGACCTG 962
QY 813 GACCGTTGGTTCCATCACTGCCCTCCCAATAACAGTTTCCTTCGCTTGACGACAGACC 872
Db 963 GACTGCGACGTACGCGACTGCAGACCCATCTATGAGTTCCATGGCTGTACGAGAGAA 1022
QY 873 ACCAGAGTGTCTGTACCTCGCTACAACTCAGATAGCCCAAGTACTACAGAGAAAC 932
Db 1023 A-----ATCTCTCCAGGCTTCAACTTCAGGTTTGCAGGCACATCTGTGGAGAC 1073
QY 933 AATGTTGAGAAACGCACTCTGATANAAGTCTTCGGGATCCGTTTGTGACATCTGTGTTT 992
Db 1074 GGGACCACTACCGTCACTCTTCAAGGTTTGGGATTCGCTTTCATCTCTGTGGAC 1133
QY 993 GGCACGGGAGGAGAAATTTGACATATCCAGCTGGTTGTGTACATCGGCTCAACCCCTCC 1052
Db 1134 GGCAGGGCGGGAAGTTTGACATCATCCCTACAATGACCACCATCGCTCTGGAATTGGC 1193
QY 1053 TACTTCGGTCTGGCCCTGTGTTGTCATCGACTTCCT 1087
Db 1194 ATCTTTGGGTGGCCACAGTCTCTCTGTGACCTGCT 1228

```

RESULT 15

AAV89619

ID AAV89619 standard; cDNA; 294 BP.

XX

AAV89619;

XX

DT 15-FEB-1999 (first entry)

XX

DE EST clone CO390.

XX

KW Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
 KW tissue growth; activin; inhibin; chemotaxis; chemokinesis; hemostatic;
 KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
 KW gene therapy; ss.

OS	Homo sapiens.
PN	W09845436-A2.
PD	15-OCT-1998.
PF	10-APR-1998; 98WO-US06955.
XX	10-APR-1997; 97US-0838821.
XX	(GEM) GENETICS INST INC.
PA	Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI	Racie LA, Spaulding V, Treacy M;
XX	WPI; 1999-070077/06.
XX	New polynucleotides encoding human secreted proteins - derived from
PT	e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT	ovary, pituitary, retina and colon cDNA libraries.
XX	Claim 1; Page 276; 618pp; English.
XX	The present sequence represents a human expressed sequence tag (EST).
CC	The polynucleotide, which is a secreted EST, and the encoded protein
CC	are predicted to have useful biological activities which would make
CC	them suitable for treating, preventing or ameliorating medical
CC	conditions in humans and animals, although no supporting data is
CC	given. Suggested activities include nutritional activity, immune
CC	stimulating or suppressing activity, haematopoiesis regulating
CC	activity, tissue growth activity, activin/inhibin activity,
CC	chemotactic/chemokinetic activity, haemostatic and thrombolytic
CC	activity, receptor/ligand activity, anti-inflammatory activity,
CC	cadherin/tumour invasion suppressor activity, tumour inhibition
CC	activity. The polynucleotide may also be useful for gene therapy.
XX	
SQ	Sequence 294 BP; 81 A; 72 C; 68 G; 73 T; 0 other;
	Query Match 10.6%; Score 196.4; DB 20; Length 294;
	Best Local Similarity 98.5%; Pred.No. 9e-44;
	Matches 197; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY	576 AGTCCGAAACCTCAGCTGTGCTCATCAAGAACAATATCGACTTCGCCGGCCACACTAC 635
Db	30 AGTCGAAAACCTCAGCTGTGCTCATCAAGAACAATATCGACTTCGCCGGCCACACTAC 89
QY	636 ACCACGAGAACATCTCTGCCAGTTTAAACATCACCTGTACCTTCCACAGACTCAGAAAT 695
Db	90 ACCACGAGAACATCTCTGCCAGTTTAAACATCACCTGTACCTTCCACAGACTCAGAAAT 149
QY	696 CCACAGTGTCCTATTTCGCAGTAGGAGACATCTCCGAGAAACAGCGCAATAATTTTCA 755
Db	150 CCACAGTGTCCTATTTCGCAGTAGGAGACATCTCCGAGAAACAGCGCAATAATTTTCA 209
QY	756 GATKGGCAATTCAGGGGGG 775
Db	210 GATGGAATTCAGTTGG 229

Search completed: July 18, 2003, 16:54:23
Job time : 463 secs

Db 517 CGGTGGAGGATGACACACACGTCGCCAACCTGCTTTTAAAGGCTGCAAGAACTTCA 576
QY 592 CTGTGCTCATCAGAACAAATATCGACTTCCCGGCGCACAACTACACACAGAGAAATCC 651
Db 577 CTCTTTGGTTAGACACACATCTGGTATCCCAATTTAATTTACGACAGAGAAATCC 636
QY 652 TGGCAGGTTTAAACATCACT-----TGTACCTTCCACAAAGACTCAGAAATCCAC 699
Db 637 TTCCAAATCACCACACTTACCTCAAGTCGTGCTATTTATGATGCTAAACACAGATCCCT 696
QY 700 AGTGTCCATTTTCGACTAGAGACATCTTCGGAACACAGGCGATTTTTCAGATG 759
Db 697 TCTGCCCCATATCTCGTCTTGGCAAAATAGTGGAGAACGACGACACGGTTTCCAGGACA 756
QY 760 KGCAATTCAGGCGGGAATATGAGCATCTACGATCTACGAGCTGCAAGCTAGACCGTT 819
Db 757 TGGCGGTGAGGAGGACATCATGGGCATCCAGTCAACTGGGACATGCAACCTGGACAGAG 816
QY 820 GGTTCATCACTGCCCTCCCAATACAGTTTCCCTCGCTTGACGACAAAGACACCAACG 879
Db 817 CGGCTCCCTCGTTCGCCAGGTACTCTTCCGCGCTCGATACACGGGACGTTGAGC 876
QY 880 TGTCTCTTACCTGGCTACAACTTCAGATACGCCAAGTACTACAGGAAACAAATG--- 936
Db 877 ACAACCTATCTCTGCTACAAATTTTCAGTTTGCCTAAGTACTACAGAGACCTGGCTGGCA 936
QY 937 TTGAGAAACGACTCTGATAAAGCTTCGSGATCGTTTTCAGATCTTGGTTTGGCA 996
Db 937 ACAGAGCGCGACGCTCATCAAGGCTATGGCATCGCTTCGACATCATTTGTTTGGGA 996
QY 997 CCGAGAGAAATTTGACATTTCCAGCTGGTGTGTGACATCGCTCAACCTCTCCCTACT 1056
Db 997 AGCAGGAAATTTGACATATCCCATATCCCATATGATGATGATGATGATGATGATGAT 1056
QY 1057 TCGGTGCGGCTGTGTGTATGACATCTTCGATCTTCCTATC 1091
Db 1057 TAGCATGGCGCGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1091

RESULT 5

US-08-750-134A-6
; Sequence 6, Application US/08750134A
; Patent No. 5985603
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750.134A
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1997 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-750-134A-6

Query Match 12.7%; Score 234.6; DB 2; Length 1997;
Best Local Similarity 55.5%; Pred. No. 6.8e-59;
Matches 585; Conservative 5; Mismatches 429; Indels 36; Gaps 6;

QY 55 TTTTCCAGTATGAGACGACAAAGTCTCATCGGATCCAGAGCATGAATATATGGCAACATTA 114
Db 135 TGTTCCGATACGACAGCGCGGCATCGTCTATCCGACGCGTAAGTGGGGCTCATGA 194
QY 115 AGTGGTTCTTCACGATGATCATCTTTCCCTACG---TTTGGCTTTCTCTGTGTAGTGA 171
Db 195 ACCCGCGGTGAGCTGCT 254
QY 172 AGCTGTACGAGCGGAAAGAGCTGTCTCATCTGTCACACCAAGCTGAGGGGATAG 231
Db 255 AGGCTTACCAAGGAAACGAGTCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 314
QY 232 CAGAGGTGAAAGAGGAGATCTGAGAGATGAGTGAAGAGTGTGTCACAGTGTCTTTG 291
Db 315 CTGTGACCAAC-----ACCTCTCAGCTTGAATTCGGATCTGGGACGCTGGGACATG 368
QY 292 ACACCGCAGACTACACTTCCCTTTGAGGGGAACTCTTTCTTCTGTGTGAGCAAACTTC 351
Db 369 TGATTCCAG-----CTCAGGAGGAAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 416
QY 352 TCBAACAGAGAGCCCAAGAGCAGCGGTGTGTCCGAGTATCCACCCGAGGACGCTCT 411
Db 417 TTGTCCCGTGAACACAGACAGACAGACACTGTCCAGAGATCTCTGATGAAGACCAAGCA 476
QY 412 GTTCTCTGACGAGGTGTGTAAGAGGATGAGTGAACCGCAGACAGAAAGAAATTCAGA 471
Db 477 GTAATTCAGAGCGCGACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 536
QY 472 CCGAAGGTGTGTATGATGAGAGGAAACAGAGACCTGTGAAGTCTCTCTCTCTCTCTCT 531
Db 537 CTGGAAGATGTGTCT 596
QY 532 CCATCGAGGAGTGGAGAGGCGCCCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 591
Db 597 CGGTGGAGAACGACTGTGGCTGCGCAAGCGCGCTTTCTTAAAGGCTGCAAGAACTTCA 656
QY 592 CTGTGCTCATCAAGAAATATCGACTTCCCGCGCACAACTACACACAGAGAAACATCC 651
Db 657 CCTCTTTGTTAAGAACACATCTGTTACCTCCCAAGTTTAACTTCAGCAAGAGGACATCC 716
QY 652 TGGCAGGTTTAA-----ACATCTGTGTACCTTCCACAGACTCA---GAATCCAC 699
Db 717 TCCCAACATCACACGCT 776
QY 700 AGTGTCCATTTTCGACTAGGAGACATCTTCGAGAGAAACAGGCGATTTTTCAGATG 759
Db 777 TCTGCCCATATTTCCGTCTTGGCAACATCTGGGGGACGCGGACATAGCTTCCAGGAGA 836
QY 760 KGCATTTCCAGGCGGAATATATGGCATCTGAGTCTTCTGAGCTGCAACCTAGACCGTT 819
Db 837 TGGCAGTTGAGGAGGACATCATGGGTATCCAGATCAAGTGGGACTGCACTGGATAGAG 896
QY 820 GGTTCATCACTGCCCTCCCAATACAGTTCCTCTGACGACAGAGACCAACAG 879
Db 897 CCGCTCTCCCTTTGCTGCCAGATATCTCTCCGCGCTGGACACCGCGGACCTGGAC 956
QY 880 TGTCTTGTACCTGGCTACAACTTCAGATACGCCAAGTACTACAGGA---AAACATG 936
Db 957 ACAATGTCTCTCTGCTACATTTTCAGTTTGCCTAAGTACTACAGGACCTGCCCGCA 1016
QY 937 TTGAGAAACGACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 996

Db 543 GGCATATGCAAGAGACAGAGTGGCTGTACCCCTGGGAAAGGCCCAAGAGGCCCAAGC 602
QY 465 ATTACAGCGGAGGTGTAGTATGAGAGGAAACAGAGACTGTGAGTCTGTCC 524
Db 603 ATCCGACGGGCAAGTGTGGCTTCAAGACACTGTGAAGAGTGTGAGTCTTTGGC 662
QY 525 TGGTGGCCATCGAGGCAAGTGTGAAGAGGCCGCCGCTGTCTTGAACAGTGCAGAA 584
Db 663 TGGTGGCCGCTGAGAGTGTGAGAGCATCCCGGCTGTCCCTTCCGAGAGGCCGAG 722
QY 585 AACTTCACTGTCTCATCAAGACAATATGAGTCTCCCGGCAACACTACACAGAGA 644
Db 723 AACTTCACTTCTTTTCAAGACAGCATCAGCTTCCAGGCTTCAAGGTCAACAGGCG 782
QY 645 AACATCTGCCAGTTTAAA-----CATCACTTGTACTTCCACAGACTCAG 692
Db 783 AACTGTGGAGAGGTGAATGTGCCACATGAGACCTGCTCTTTCACAGACCTG 842
QY 693 AATCCACAGTGTCCCATTTTCCGACTAGGAGACATCTCCGAGAAACAGGCGGATAATTT 752
Db 843 CACCCCTGTGCCAGTCTTCCAGCTTGGCTAGGTGGTGCAGAGTCAAGGCGAAGCTTC 902
QY 753 TCAGATGKGCAATTCAGGCGGAATTAAGGCAATGAGATCTACTGGGACTCAACCTA 812
Db 903 AGCACCTTGGCTGAGAGAGGTGGAGTGTGGCATCACATCGACTGGCACTGTGACCTG 962
QY 813 GACCGTGTGTCCATCATCTGCRPCCAATACAGTTCCTGCGCTTGAGCAGACAGCC 872
Db 963 GACTGCGAGTACGCACTGACACCATCTATGAGTTCATGAGGCTGTACGAGAGAAA 1022
QY 873 ACCAACGTCTCTTGTACCTGGCTCAACTTCAGATAGCCAAAGTACTACAAGGAAAC 932
Db 1023 A-----ATCTCTCCAGGCTTCAACTTCAGTGTGGCAGGCACTTTGAGAGAC 1073
QY 933 AATGTTGAGAAAGGACTCTGATAAAGTCTTCGGGATCCGTTTGTGATCTCGGTTTT 992
Db 1074 GGAACCAACTACCGCTCACTCTTCAAGGTGTGGGANTTGGCTTGTGATCTCGTGGAC 1133
QY 993 GGCACCGGAGGAAATTTGACATTCACAGCTGGTGTGTATCGCTCAACCCCTCC 1052
Db 1134 GCAAGCGGGAAGTTTGACATCATCCCTACAAAGACACCATCGGCTCTGGAATGGC 1193
QY 1053 TACTTCGGTCTGGGCGCTGTGTTCATCGACTTCCT 1087
Db 1194 ATCTTTGGGTGGCCACAGCTTCTGTGACCTGCT 1228

RESULT 9

US-08-750-134A-4

Sequence 4, Application US/08750134A

Patent No. 5985603

GENERAL INFORMATION:

APPLICANT: VALERA, SOLEDAD

APPLICANT: BUELL, GARY

TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/750,134A

FILING DATE: 22-JAN-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: CRAWFORD, ARTHUR C.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 1430-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4006
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: rat P2x from vas deferens
US-08-750-134A-4

Query Match 8.6%; Score 159.6; DB 2; Length 1837;

Best Local Similarity 50.7%; Pred. No. 7.8e-37;

Matches 434; Conservative 6; Mismatches 395; Indels 21; Gaps 2;

QY 244 AGGAGATCGYGGAGAAAGTGAAGAAGTGTGTGCACAGTGTCTTTGACACCGCAGACT 303
Db 418 AGGGCTTGGCTGTGACCCAGCTCCAGGGCTGGGACCCAGGTCTGGGAGCTGGCTGACT 477
QY 304 ACACCTTCCCTTTGAGGGGAGTCTTCTTCTGTGATGACAAACTTTTCAAAACAGAG 363
Db 478 ATCTCTCCACAGACAGGGGACAGCTCCTTTGTAGTTATGACCAACTTCATCGTGAACC 537
QY 364 GCCAAGAGCAGCGGTGTGTCCCGAGTATCCACCGCAGGAGCCTGTCTCTCTGACC 423
Db 538 CTCAGCAGACTCAAGGCCATGTGCGAGAACCCAGAGGTGGCAATATGCCAGGATGACA 597
QY 424 GAGTTGTTAAAGGGATGATGACCCGAGAGCAAGAAAGTATTCAGACCGAGGTGG 483
Db 598 GTGGCTGCACTCCAGGAAAGCAAGAAAGGAAAGCCAAAGTATTGCGACAGCAACTGTG 657
QY 484 TAGTATGAGGGGAACCAAGAGACCTGTGAAGTCTCTGCTGTGTGCCATCGAGGCGAG 543
Db 658 TGGCTTCAAGGGCACTGTGAGACATGTGAGATCTTTGGTTGGTCTCTGTGAGAGTGG 717
QY 544 TGAAGAGAGCCCGCGCTGTCTCTTTGAACAGTGCAGGAAACTTCATCTGTCTCATCA 603
Db 718 ATGACAAGATCCAGGCCCTGCTCTTCTTCTGTGAGCTGAGAACTTCACCCCTCTCATCA 777
QY 604 AGAACAATATCAGTTCGCCGCGCCCACTATACACACAGAGAAACATCCTGCCAGGTTAA 663
Db 778 AAAACAGCATCAGCTTCCAGGCTTCAAGGTCAACAGGCGCAACCTGCTGAGAGGAGTGA 837
QY 664 ACATCACTTGTGTA-----CCTTCCACAAGACTCAGAAATCCACAGTGTCCCATTT 711
Db 838 ACGGCACCTTACATGAGAAAGTGGCTCTATCAAAAGATTCAACACCCCTGTGCCAGTCT 897
QY 712 TCCGACTAGGAGACATCTCCGAGAAACAGGCGGATAATTTTCAGATGKGCAATTCAGG 771
Db 898 TCAACCTTGGCTATGTGTGGAGAGTCAGGCCAGGACTTCCGAGCAGCTTGTGTGAGAAGG 957
QY 772 GCGGAATAATGGCAATTCAGATCTACTTGGGACTGCAACTAGACCTGAGTGTGTCTCACT 831
Db 958 GTGGGTGGTGGTATCACCATTGACTGGAAAGTGTGATCTGGACTGGCAGTTCGGCACT 1017
QY 832 GCCTCCCAATATACAGTTCCTCGCTTGAAGAGAGCAAGAACCAACAGTGTCTCTGTACC 891
Db 1018 GCAACCCATCTACAGTTCACAGTTCACAGGACTATGAGGGAGAGAAC-----TGTCTC 1068
QY 892 CTGGCTTACAACTTCAGATGAGCCCAAGTACTACAAGAAACAAATGTTGAGAAACGAGT 951
Db 1069 CAGGCTTCAACTTCAGATTTGCCAGGCACTTGTCTCAGAAATGGGACAAACCGTCTGCTACC 1128
QY 952 TGATAAAAGTCTCGGATCCGTTTGTGACATCCTCGTTTGGCACCGGAGGAAATTTG 1011
Db 1129 TCTTCAAGGTGTTGGGATTCACCTTTGATATCCTTGTGATGCGCAAGGCTGGGAGTTTG 1188

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QY 1012 ACATTATCCAGCTGGTGTGTACATCGGCTCAACCCCTCTCCCTACTTGGTGGCCCTG 1071
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Db 1189 ACATCATCCCTACTATGACTACTATCGGTTCTGGGATTCGGCATCTTTGGAGTGGCCACAG 1248
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QY 1072 TGTTCATCGACTTCCT 1087
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Db 1249 TGCCTTGTGATCTCT 1264
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RESULT 10
US-09-363-745-4
; Sequence 4, Application US/09363745
; Patent No. 6194162
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,745
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,134
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1837 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: rat P2x from vas deferens
; US-09-363-745-4

Query Match 8.6%; Score 159.6; DB 4; Length 1837;
Best Local Similarity 50.7%; Pred. No. 7.8e-37;
Matches 434; Conservative 6; Mismatches 395; Indels 21; Gaps 2;

QY 244 AGGAGATCGYGGGAATGGAGTGAAGAAGTTGGTGACAGTGTCCTTGTGACACCCGAGACT 303
|||||
Db 418 AGGGCTTGCTGTGACCCAGCTCCAGGCGCTGGGACCCAGGCTGGGACGTGGCTGACT 477
|||||
QY 304 ACACATCCCTTTGCGAGGGAAGTCTTTCTTCGTGANGACAACACTTCTCAACACAGAAG 363
|||||
Db 478 ATGTCTTCCAGCAGCAGGGGAGCTCTCTTTGTAGTTATGACCAACTTCATCGTGACC 537
|||||
QY 364 GCCAGAGACGCGTGTGTCCCGAGTATCCACCCCGAGAGCGCTCTCTCTCTGACC 423
|||||
Db 538 CTCAGACACTCAAGGCCATTTGTGCAGAGAACCCAGAGAGTGGCATATGCGAGGATGACA 597
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QY 424 GAGGTGTGTAAGAGGATGGATGGACCGCGCAGAGCAAGGAATTCAGACCGGAGGTGTG 483
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Db 598 GTGCTGCTCACTCCAGGAAAGCAGAAAGGAAAGCCCAAGGATTCGACAGGCAACTGTG 657
QY 494 TAGTATATGAGAGGAAACAGAGACCTGTGTGAATGTCCTGCTGGTGGCCCATGAGAGCAG 543
|:|||||
Db 658 TGCCCTTCAATGGCACTGTGAAGACATGTGAGATCTTTGGTTGGTGTCTCTGAGAGGTG 717
|||||
QY 544 TGAAGAGGCCCCCGGCTCTCTCTTGAACAGTGCAGAAACTTCACATGTGTCATCA 603
|||||
Db 718 ATGACAAGATCCCAAGCCCTCTCTCTCTGAGAGTGAAGACTTACCCCTCTCTCA 777
|||||
QY 604 AGAACAATATGACTTTCCCGGCCACAACTACACACGAGAAACATCTCTGCAAGTTAA 663
|||||
Db 778 AARACGATCATGCTTCCACGCTTCAAGGTCACAGGCGCAACCTGTGAGAGGTGA 837
|||||
QY 664 ACATCACTTGTA-----CCTTCCACAGACTCAGAAATCCAGTGTCCCATTT 711
|||||
Db 838 ACGCACCTACATGAAGAAGTGCCTCTATCACAAGATTCACACCCCTGTGCCAGTCT 897
|||||
QY 712 TCGAGCTAGGAGACATCTCCGAGAAACAGCGCATATTTTCAGATGKGCATTCAGG 771
|||||
Db 898 TCAACCTTGGCTATGTGGTGGAGAGTCAGGCCAGGACTTCGCGAGCCTTCTCTGAGAGG 957
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QY 772 GCGAATAAATGGGCATTTGAGATCTACTGGGACTGCAACCTAGACCGTTGGTTCATCACT 831
|||||
Db 958 GTGGGTGGTGTGATATCACCATTGACTGGAAGTGTGATCTGGACTGGCAGCTTGGC 1017
|||||
QY 832 GCGTCCCAATACAGTTTCCTGCGCTTGACGACAGACCAACAGTGTCTCTGTAC 891
|||||
Db 1018 GCAAAACCATCTACCAAGTTCCACGAGCTGTATGGGAGAGAAAC-----TGTCTC 1068
|||||
QY 892 CTGGCTACAACTTCAGATAGCCCAAGTACTACAAGGAAACAACTTTGAGAAACGGACT 951
|||||
Db 1069 CAGGCTTCACCTTCAGATTTGCCAGGCAATTCGTGCGAATGGGCAACCGTCTGAC 1128
|||||
QY 952 TGATAAAAGTCTTCGGGATCCGTTTTCAGATCTCTGCTGCTTTGGCCACCGAGAAATTTG 1011
|||||
Db 1129 TCTTCAAGGTGTTGGGATTCATTTGATATCTTTGGATGGCAAGCTGGGAAGTTTG 1188
|||||
QY 1012 ACATATCCAGCTGGTGTGTACATCGGCTCAACCCCTCTCTCTCTCTCTCTCTCTCT 1071
|||||
Db 1189 ACATCATCCCTACTACTACTACTATCGGTTCTGGGATTCGGCATCTTTGGAGTGGCCACAG 1248
|||||
QY 1072 TGTTCATCGACTTCCT 1087
|||||
Db 1249 TGCCTTGTGATCTCT 1264
|||||

RESULT 11
US-09-191-136-13
; Sequence 13, Application US/09191136B
; Patent No. 6214581
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Lynch, Kevin J.
; APPLICANT: Burgard, Edward C.
; APPLICANT: Van Biesen, T.
; TITLE OF INVENTION: Nucleic Acids Encoding A Functional
; TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
; FILE REFERENCE: 6293.US.P1
; CURRENT APPLICATION NUMBER: US/09/191,136B
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: US 09/008,526
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 09/008,185
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 60/071,298
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: US 60/071,669
; EARLIER FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
```


ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/750,134A
FILING DATE: 22-JAN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR C.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 1430-116
TELEPHONE: (703) 816-4006
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1753 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-750-134A-8

Query Match
Best Local Similarity 52.6%; Score 140.2; DB 2; Length 1753;
Matches 457; Conservative 3; Mismatches 376; Indels 33; Gaps 6;

876 TCTGGTATTAGATCGGCTGGGTGCGGATCTAGACAAGCCCTGGACCACTGCATCCC 935
839 CAATACAGTTTCCTCGCTTTCAGACAGACACCAACAGTGTCTCTGACCTGGCTA 898
936 TAAATATTCTCTACTCGGCTGGATGAGTTCTCTGAGAAAAGCAGTGTCTCCCTGGCTA 995
899 CAACTTCAGATAGCCCACTACTACAA--GGAACAATGTTGAGAAACGACTCTCAT 955
996 CAACTTCAGGTTTGGCAATATAAGATGGAGAGCGGAGGATACCGCACTCTCT 1055
956 AAAAGTCTTCGGATCCGTTTTCACATCCTGGTCTTTGGCACCGGAGGAAATTTGACAT 1015
1056 GAGGCTTTGGCATCCGCTTGTGATGCTGTATATGGAACGCTGGAAGTCAACAT 1115
1016 TATCAGCTGTGTGTATACATCGGCTCAACCTCTCTCTCTCTCGGCTCGGCTGTGT 1075
1116 CATCCCAACATTATCAGCTCGTGGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1175
1076 CATGCACTTCTCATCGACASTTACTCCA 1104
1176 CTGTGACATCATCTCTCTCAATTTCTCTCA 1204

RESULT 14
US-09-363-745-8
Sequence 8, Application US/09363745
Patent No. 6194162
GENERAL INFORMATION:
APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,745
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/750,134
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR C.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 1430-116
TELEPHONE: (703) 816-4006
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1753 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-363-745-8

Query Match
Best Local Similarity 52.6%; Score 140.2; DB 4; Length 1753;
Matches 457; Conservative 3; Mismatches 376; Indels 33; Gaps 6;

254 GGAGATGGAGTGAAGTGTGTCACAGTGTCTTTGACACCGGAGACTACCTTCCC 313
351 GGTGAAGGCTTGGGCGGTATGCCAACAGACTCATGAGCTGTGGATATGACCCC 410
314 TTTCAGGGAACCTCTTCT--TCGTGATGACAACTTTCTCAAAACAGAGGCCAAGA 370
411 ACCCGAGGACCTCTGTCTTGTATCATCAACCAAAATGATGTTTACTGAAATCAAT 470
371 GCAGCGTGTGTCGCGGATATCCACCGGAGACCTCTGTCTCTCTGACGAGGTG 430
471 GCAAGGATCTGTCCAGAAAT--GAAAGAGAGTACCGCTGTGTCTGTGACAGCCAGT 527
431 TAAAAGGATGGATGACCGGAGCAAGAAATTCAGACCGGAGAGTGTGTAGTGA 490
528 TGGGCTGACG-----CTTCCAGTGGGGGATCTCACCAGCGCTGCTGGACTA 581
491 TGAAGGAACAGAAAGACTGTGAAGTCTCTGCTGTCGCCATCGAGGAGTGAAGA 550
582 CAGCTCTGTTCTCGGACCTGTGAGATCCAGGCTGTGTCCTCA-----CTGAGGTGA 635
551 GCGCCCGGCGCTCTCTCTGACAGCTGCGGAAATTCACGTCTCTCTATCAGAACAA 610
636 CACCGTGAGATGCTATCATGATGAGGCTGAGAACTTCACCAATTTTCATCAAGAACAG 695
611 TATGACTTCCGCGGACCAACTACACCGAGAAACATCTCCAGAGTTTAAACATCAC 670
696 CATCGTTTCCCTCTCTCTCACTTTGAGAGGAGAACTCTCTGCTTAACCTCACGAC 755
671 T-----TGTAACCTTCCACAGACTCAGAAATCCACAGTGTCCCATTTTCCGACT 718
756 GGACATAAGAGGTGCGCTTCCACCTCAAGAGGCCCAATTTTGCCCATCTTGAGGT 815
719 AGGAGACATCTCCGAGAACAGGCGATATTTTCAGATGKGGAATTCAGGCGGAGAT 778
816 AGGGATGTGTTAAGTTGCTGGACAGATTTTGCCAAAGCTGGCCCGCAGCGGTGGGT 875
779 ATGGGCAATTGATCTACTGAGTGTCAACTAGACCGTGTGTCTTCCACTCTGCTCC 836

351	GGTGAAGAGC	TTCGGGCGCTATGCCAACAGAGCTCATGGACGCTGTCGGATATGTGACCCC	410
314	TTTCAGGGGA	ACTCTTTCT---TCGTGATGACAAACTTTCTCAAAACAGAGGCGCAAGA	370
411	ACCCAGGC	CACTCTGTCTTTGTATCATCACCACAAATGATCGTTACTGAAATCAAT	470
371	GCACGGTTGT	GTCCCGAGTATCCACCCGCGAGGACGCTCTGTTCCTCTGCACCGAGGTG	430
471	GCAGAGTCT	GTCCAGAGAT---GAAGAGAAGTACCGCTGTGTCTCTGCAGCGCAGTG	527
431	TAAAAAGGAT	GGATGGACCGCAGAGCAAAAGGAATTCAGACCGGAGAGTGTGTAGTATTA	490
528	TGGCGCTGA	CG-----CTTCCAGGTGGGGGATCCTCACGGCGCGTGCCTGAAGCTA	581
491	TGAAGGAAC	CAGAGACCTGTGAAGTCTCTGCCTGTGCGCCATCGAGCGCAGTGGAAAGA	550
582	CAGCTGTGT	CTCCGGCACTGTGAGATCCAGGGCTGTGTGCCCA-----CTGAGGTGGA	635
551	GGCCCCCG	CGCTCTCTGTGACAGTGCCTGAAGACTGCCGAAGACTTCACTGTGCTCATCAAGACAA	610
636	CACGTGGA	GTCCCTATCATGATGGAGGCTGAGAACTTACCATTTCATCAAGAACAG	695
611	TATCGACTT	CCCCGCCACAACTACACCAGAGAAACATCCTGCCAGGTTTAAACATCAC	670
696	CATCCGT	TTTCCCTCTCTTCAACTTGAAGAGGAAACCTCTGCCTTAACCTCACCGACAA	755
671	T-----	-----TGTACCTTCCACAGACTCAGAACTCCAGCTCCAGTGTCCCATTTCCGACT	718
756	GGACATAA	AGAGAGTCCCGCTTCCACCTGAAAGGCCCATTTTGGCCCATCTTGAGSGT	815
719	AGGAGACAT	CTTCOCAGAAACAGCGGATATTTTTCAGATKGSCAATTCAGCGGGGAT	778
816	AGGGATGT	GTAGTTGCTGGACAGGATTTGCCAAGCTGGCCCGCAGCGGTGGCGT	875
779	ATGGGCA	TGAGATCTACTGGGACTGCCAACCATAGACGTTGTTCCATCTACGCTCC	838
876	TCGGGTAT	TATAGATCGGCTGGGTGTGCGATCTAGACAAGSCCTGGGACGAGTCATCCC	935
839	CAATACAG	TCTTCCTCGCTTCAGCAACAGCACACAGGTGTCTTGTACCTGGCTA	898
936	TAAATAT	CTCTACTCGCTGGATGAGTTCTGAGAAAAGACAGTGTTCCTCCCTGGCTA	995
899	CAACTTC	CAGATACGCCAAGTACTACAA---GGAAACAAATGTTGAGAAACGCACTCTGAT	955
996	CAACTTC	AGGTTTGCACAAATACATAAGATGAGAAACGGCAGCGAGTACCGCACACTCCT	1055
956	AAAGTCT	TCGGGATCCGTTTGACATCTCGTTTGGCACCGGAGGAAAAATTGGAAT	1015
1056	GAAAGGT	TTTGGCATTCGCTTTGATGTGTGATATATGGAAACGCTGGCAAGTTCAACAT	1115
1016	TATCCAG	CTGGTTGTGTACATCGGCTCAACCCCTCCCTACTCGGCTCTGGCCRCGCTGT	1075
1116	CATCCCC	ACCATATACCTAGCTCGGTGGGGCCCTTCATCTCTGTGGAGTGGGCACGTGCT	1175
1076	CATCGACT	CTCTCATFCGACAAATTACTCCA	1104
1176	CTGTGCAT	CACTCTGTCTCAATTTCTCTCA	1204

RESIST 15

RESULT IS
DS-09-191-608-14

US-09-191-608-14
: Sequence 14. Application US/09191608: sequence 14, Appl. No. 6242216
: Patent No. 6242216; FACILE NO. 0242210
; GENERAL INFORMATION:

APPLICANT: Lynch, Kevin J.

APPLICANT: BURGARD, Edward C.

APPLICANT: Metzger, Randy E.

APPLICANT: Niforatos, Wende

; APPLICANT: Toulmà, Edward B.

APPLICANT: Van Biesen, T.

); ALBERT, van Biesen/ 1.
; TITLE OF INVENTION: Nucleic Acids Encoding a Functional

TITLE OF INVENTION: Human Purinoreceptor P2X2 and P2X4 And Methods of Production

; TITLE OF INVENTION: And Use Thereof

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; FILE REFERENCE: 6394.US.P1
; CURRENT APPLICATION NUMBER: US/09/191,608
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1421
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-191-608-14

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Query Match	7.6%;	Score 140;	DB 4;	Length 1421;
Best Local Similarity	52.3%;	Prod. No. 3.9e-31;		
Matches 402;	Conservative	5; Mismatches 340;	Indels 21;	Gaps 4;
QY	398	CCGACGAGCGCTCTGTTCCTCTGACCGCGAGGTGTAAAGGGATGGATGGACCCGACAG	457	
Db	398	CCACAGCCACTGCTCTCCGACGCCAGCTGCTGGCTGGGAGCTGGACATGCTGGG	457	
QY	458	CAAGAGTAATTCAGACCGGAGGTGTGAGTRYAT---GAAGGGACCAAGAACCTTGGA	514	
Db	458	AAAGCGCCTGAGACCGGGCGCTGTGTGCCCTATTACGAGGGGCCCTCAAGACCTGGG	517	
QY	515	AGTCTCTGCTGGTGGCCCATTCGAGGACAGTGGAGAGGCCGCCCGCGCTGCTCTTGA	574	
Db	518	GGTGTTCGGCTGGTGCCC---GGTGGAGATGGGCGCTCTGTGAGCCAAATTTCTGGGTAC	574	
QY	575	CAGTGGCCGAAAATTCACCTGTGCTCATCAAGAACAAATATCGACTTCGCCGGGCCAACCTA	634	
Db	575	GATGGCCCCAATTCACCATTCCTCATCAGAACAGATCCACTACCCCAATTCACCTT	634	
QY	635	CACACGAGAACATCTCTGCAGGTTTAAAC-----ATCATTGTACTTCCACAA	685	
Db	635	CTCCAAGGCAACATCGCGCGACGACACAGCGGGTACCTGAAGCGTGCACCTTCCACGA	694	
QY	686	GACTCAGATTCACAGTGTGCCATTTTCCGACTAGSAGACATCTTCGAGAACACAGGCGA	745	
Db	695	GGCTTCGACCTCTACTGCCCATCTTTCAGCTGGGCTTTATCGTGGAGAGGCTGGGGA	754	
QY	746	TAATTTTCAGATGKGGCAATTCAGGCGCGAATAATGCGCATTTAGATCTACTGGGACTG	805	
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QY	806	CAACCTAGACCGTGTGGTTCATCTACCTGCCCTCCAAAATACAGTTTCCCTGCGCTTACGA	865	
Db	815	TGACCTGGACCTGCTGTGATCGGAGTGCACACCCCAAGTACTCTCTCGGAGGCTTGACC	874	
QY	866	CAAGACCCAAACGTGTCTTGTACCTGGCTACAACTTCAGATACGCCAAGTACTACAA	925	
Db	875	CAACG-----ACGTGCGCTCGCTCGACGCTACAACCTCAGGTTGGCCAATACTACAA	928	
QY	926	GGAAAACAATGTTGAGAACCGACTCTGATATAAGTCTTCGGGATTCGCTTTTGGACATCT	985	
Db	929	GATCAATGGCAACACACCCCGACGCTCATCAAGCCCTACGGGATCGCATTTGACGTAT	988	
QY	986	GGTTTTTGGCACCGGAGGAAAAATTGACATTAATCCAGCTGGTGTGTACTCGGCTCAAC	1045	
Db	989	TGTGCATGGACAGCGCGGAGATTCACGCTGATTTCCACCAATTATTAATCTGGCCACAGC	1048	
QY	1046	CCTCTCTACTTGGGTGGCCRCCTGTGTTTCATCTGCACTTCCTCATCGACASTTACTCCAG	1105	
Db	1049	TCTGACTTCGCTGGGGTGGCTCCTTCTCTGTGCGACTTGGATCTGTGTAACTTATGAA	1108	
QY	1106	TAATCTGTCTGCTGCCATTAATTAATTCCTGTGGTGGAAAGTGTGTGACGC	1153	
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Job time : 103 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 18:14:54 ; Search time 422 Seconds
(without alignments)
9058.627 Million cell updates/sec

Title: US-09-977-221-2

Perfect score: 1853

Sequence: 1 aaacagcaggaggagct.....cgtctgtaatccacatttt 1853

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
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2	1837.8	99.2	2164	15	US-10-175-523-191
3	237.	12.8	1389	11	US-09-833-082-1
4	203.8	11.0	2633	11	US-09-969-347-225
5	147.4	8.0	4900	12	US-09-977-221-1
6	142.6	7.7	11270	12	US-09-977-221-3
7	113.6	6.1	515	12	US-09-918-995-31290
8	102.6	5.5	1956	11	US-09-864-864-331
9	94.6	5.1	423	11	US-09-864-864-254
10	90.8	4.9	276	11	US-09-960-352-11220
11	89.8	4.8	698	15	US-10-027-632-103774
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13	57.2	3.1	458	12	US-09-918-995-5505
14	52.8	2.8	229	11	US-09-998-598-1742
15	51.2	2.8	941	11	US-09-764-847-250
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17	43.6	2.4	2511	15	US-10-157-031-61	Sequence 61, Appl
18	42.8	2.3	817	15	US-10-027-632-130520	Sequence 130520,
19	42.8	2.3	817	15	US-10-027-632-130521	Sequence 130521,
20	42.6	2.3	2302	11	US-09-764-868-445	Sequence 445, App
21	42.6	2.3	2302	12	US-09-955-999-12	Sequence 12, Appl
22	42.2	2.3	2273	10	US-09-853-386-110	Sequence 110, Appl
23	40.8	2.2	31949	12	US-09-764-891-8098	Sequence 8098, Ap
24	40.8	2.2	32186	12	US-09-764-891-8099	Sequence 8099, Ap
25	40.6	2.2	1083	15	US-10-156-761-4116	Sequence 4116, Ap
26	40.6	2.2	9025608	15	US-10-156-761-1	Sequence 1, Appli
27	40.4	2.2	747	15	US-10-027-632-12749	Sequence 12749, A
28	39.8	2.1	3630	15	US-10-027-632-113827	Sequence 113827,
29	39.8	2.1	1691139	15	US-10-067-514-1	Sequence 1, Appli
30	39.4	2.1	133893	15	US-10-161-510-1	Sequence 1, Appli
31	39.2	2.1	188	11	US-09-867-701-2156	Sequence 2156, Ap
32	39	2.1	2187	15	US-10-156-761-352	Sequence 352, App
33	38.8	2.1	172637	10	US-09-805-458A-3	Sequence 3, Appli
34	38.6	2.1	599	15	US-10-027-632-112354	Sequence 112354,
35	38.4	2.1	854	15	US-10-027-632-7328	Sequence 7328, Ap
36	38.4	2.1	854	15	US-10-027-632-7329	Sequence 7329, Ap
37	38.4	2.1	854	15	US-10-027-632-7330	Sequence 7330, Ap
38	38.4	2.1	1049	14	US-10-146-731-358	Sequence 358, App
39	38.4	2.1	1049	15	US-10-123-155-358	Sequence 358, App
40	38.4	2.1	1864	10	US-09-770-621-3	Sequence 3, Appli
41	38.2	2.1	1721	15	US-10-027-632-97145	Sequence 97145, A
42	38	2.1	291	15	US-10-040-739-1146	Sequence 1146, Ap
43	38	2.1	460	15	US-10-175-523-30	Sequence 30, Appl
44	38	2.1	536	15	US-10-027-632-92609	Sequence 92609, A
45	38	2.1	536	15	US-10-027-632-304029	Sequence 304029,

ALIGNMENTS

RESULT 1
US-09-977-221-2
; Sequence 2, Application US/09977221
; Publication No. US20030008293A1
; GENERAL INFORMATION: JOHN EDWARD NORRIS
; APPLICANT: NORRIS, JOHN EDWARD NORRIS
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; FILE REFERENCE: PLS/009901/0283779
; CURRENT APPLICATION NUMBER: US/09/977,221
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/244,897
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: GB 0025859.0
; PRIOR FILING DATE: 2000-10-21
; PRIOR APPLICATION NUMBER: GB 0108654.5
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-977-221-2

Query Match 99.7%; Score 1846.6; DB 12; Length 1853;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAACACGAGGAGGAGGCTGTCCACCATGCGGCCCTGCTGCAGCTGCAGTGAGTGTTC	60
DB	1	AAACACGAGGAGGAGGCTGTCCACCATGCGGCCCTGCTGCAGCTGCAGTGAGTGTTC	60
QY	61	AGTATGACGACGACAAAGTCTACTCGGATCCAGACGATGATTTATGGACCATTAAGTGT	120
DB	61	AGTATGACGACGACAAAGTCTACTCGGATCCAGACGATGATTTATGGACCATTAAGTGT	120
QY	121	TCATCCACGNGATCATCTTTTCCTACGTTTCCTTCCTGCTGAGTGACAGCTGTACC	180
DB	121	TCATCCACGNGATCATCTTTTCCTACGTTTCCTTCCTGCTGAGTGACAGCTGTACC	180

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DB 181 AGCGGAAAGAGCTCTCATAGTTCGTGCACACCAAGGTGAAGGGATAGCAGAGTGA 240
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DB 241 AAGAGGAGATCGYGAGAAATGGAGTGAAGAGTGGTGCACAGTGTCTTTGACACCGAG 300
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DB 301 ACTACACTTCCCTTTCAGGGGAATCTCTTCTGTGTATGACAAATCTTCTCAAAACAG 360
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QY 481 GTGTAGTATGAGGGAACAGAGACCTGTGAAGTCTCTGCTGTGTCGCCATCGAGG 540
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QY 1021 AGCTGGTGTGTACATCGGCTCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
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DB 1441 ATAGCCCTGTCTGTGCTGCTGGAAGTGTCCCATCTCAACTCCCTGAGRGCCACA 1500
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DB 1681 GCTAGCCACCTGCGCTGCTGCTGCGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1740
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RESULT 2

US-10-175-523-191
; Sequence 191, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajau, Prithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/13795-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 191
; LENGTH: 2164

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Db	117	TGACGACAAAGATCACTCGGATCCAGAGCATGAATATGGCCACCATTAAGTGGTCTT	176			
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Db	177	CCAGTGTATCATCTTTTCTTACGTTTTCCTTCTGCTGAGTGCACAGCTGTACCAAGC	236			
QY	185	GAAGAGCCTGTCACTAGTCTGTGCACACCAAGTGAAGGGATAGCAGAGGTGAAGA	244			
Db	237	GAAGAGCCTGTCACTAGTCTGTGCACACCAAGTGAAGGGATAGCAGAGGTGAAGA	296			
QY	245	GGAGATCGGAGGAATGAGGTGAAGAAGTTGGTGCACAGTCTTTTGAACACCGCAGACTA	304			
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QY	305	CACCTTCCCTTTGCAGGGGAACCTCTTCTTCGTGATGACAAATTCAGACCGGAAGTGT	364			
Db	357	CACCTTCCCTTTGCAGGGGAACCTCTTCTTCGTGATGACAAATTCAGACCGGAAGTGT	416			
QY	365	CCAAGAGCAGCGGTTGTGTCCCGAGTATCCACCGCAGGAGCGTCTGTTCTCTGACCG	424			
Db	417	CCAAGAGCAGCGGTTGTGTCCCGAGTATCCACCGCAGGAGCGTCTGTTCTCTGACCG	476			
QY	425	AGGTTGTAAAAAGGATGGATGGACCCCGCAGACGAAGAATTCAGACCGGAAGTGTGT	484			
Db	477	AGGTTGTAAAAAGGATGGATGGACCCCGCAGACGAAGAATTCAGACCGGAAGTGTGT	536			
QY	485	AGTATATGAGGGAACACAGAGACCTGTGAGTCTCTGCTGGTGGCCCATCGAGGCAGT	544			
Db	537	AGTATATGAGGGAACACAGAGACCTGTGAGTCTCTGCTGGTGGCCCATCGAGGCAGT	596			
QY	545	GGAAGAGCCCCCGCCCTGCTCTGTGAACAGTGCAGTGTCCCAACTTCACCTGTCTCATCAA	604			
Db	597	GGAAGAGCCCCCGCCCTGCTCTGTGAACAGTGCAGTGTCCCAACTTCACCTGTCTCATCAA	656			
QY	605	GAAATATGAGTCTCCCGGCCACACTACACAGAGACATCTCTCCAGGTTTAA	664			
Db	657	GAAATATGAGTCTCCCGGCCACACTACACAGAGACATCTCTCCAGGTTTAA	716			
QY	665	CATCAGTGTACCTTCCACAAAGACTCAGATCCAGTGTCCCATTTCCGACTAGGAGA	724			
Db	717	CATCAGTGTACCTTCCACAAAGACTCAGATCCAGTGTCCCATTTCCGACTAGGAGA	776			
QY	725	CATCTCCGAGAAACAGGCGTATTTTTCAGATGKGCATTCAGGGCGGTAATGGG	784			
Db	777	CATCTCCGAGAAACAGGCGTATTTTTCAGATGKGCATTCAGGGCGGTAATGGG	836			
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Db	837	CATTGAGATCTACTGGGACTGCAACCTTAGACCGTTGGTTCCATCACTGCCTCCCAATA	896			
QY	845	CAGTTTCCRTGCGCTTGACGACAAAGACCAACGTTGTCCTTGCCTTGGCTACAACTT	904			
Db	897	CAGTTTCCRTGCGCTTGACGACAAAGACCAACGTTGTCCTTGCCTTGGCTACAACTT	956			
QY	905	CAGATAGCCCAAGTACTACAGGAAACAACTGTTGAGAAACGGACTCTGATATAAGTCTT	964			
Db	957	CAGATAGCCCAAGTACTACAGGAAACAACTGTTGAGAAACGGACTCTGATATAAGTCTT	1016			
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RESULT 3
US-09-833-082-1
; Sequence 1, Application US/09833082
; Patent No. US20020151480A1
; GENERAL INFORMATION:
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 10218
; FILE REFERENCE: WNI-227
; CURRENT APPLICATION NUMBER: US/09/833,082
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 1
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-833-082-1

Query Match      12.8%; Score 237; DB 11; Length 1389;
Best Local Similarity 54.4%; Pred. No. 4.8e-64;
Matches 574; Conservative 5; Mismatches 440; Indels 36; Gaps 4;

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QY 62 TGTTCAGTATGAGACGACGCGCGCATCGTCTCATCCGACGCGCAAGTGGGCTCATGA 121
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 122 ACCGGCGCGTCAACTCTCATCTGGCTACGTCTGGTGGTGGTGGTGGTGGTGGTGGTGG 181
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 172 AGCTGTACACGCGAAGAGCCCTGTCATCAGTCTGTGTCACACCAAGGTGAAGGGATAG 231
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QY 182 AGGCTACACGAAACTGATCTCGTGTGTCAGCTCCGTACGACCAAGGTCAAGGCGTGG 241
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QY 232 CAGAGGTGAAGAGAGATCGYGGAGATGGAAGTGAAGTGGTGCACAGTGTCTTTG 291
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QY 242 CTGTACCAACACACTCTTAACCTTGGATTCCGGATCTGGGATGGCGGATTATGTATAC 301
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QY 292 ACACGCGAGATACACCTTCCCTTTCAGGGGAACCTCTTCTCGTGTGATGACAAACTTC 351
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 302 CAG-----CTCAGGAGAAACTCCCTCTCGTCATGTGCAACCAAGTGA 343
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QY 352 TCAAAACAGAGGCGCAAGAGCAGCGGTGTGTCCCGAGTATCCCAACCGCAGGAGCTCT 411
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 344 TCCTCACCNTGAACACACAGCAGCGCTGTGCCCGGAGATCCAGATCGCACCATCTGT 403
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 412 GTTCTCTGACCGAGTGTGAAGAAGGATGATGAGACCGCAGAGCAAGGAATTCAGA 471
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 404 GTAAATCAGATGCCAGTCTACTCGCGGCTCTGCGGCAACCCACAGCAACGAGTCTCAA 463
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 472 CCGAAGGTGTGTAGTATGAAGGAACACAGAGACTGTGAAGTCTCTGCTCTGCTGCC 531
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 464 CAGGAGGTGCGTAGCTTTAAGGGTCTGTCAGACGTGTGAGGTGGGCGCTCGTGGCC 523
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 532 CCATCCAGGAGTGAAGAGGCCCCCGCCCTCTCTCTTTGAACAGTGCAGCCGAAAACTTCA 591
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 524 CGGTGGAGGATGACACACAGTCCCAACCTGCTTTTAAAGGCTGCAGAAACTTCA 583
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 592 CTGTGCTATCAGAACATATGACTTCCCGGCGCCACTACACACAGAGAAATATCC 651
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 584 CTCTTTTGGTTAAGAACACATCTGGTATCCCAAAATTTAATTTCAAGAGGAATATCC 643
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 652 TGCAGGTTTAAATCACT-----TGTACCTTCCACAGACTCAGAATCCAC 699
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 644 TTCCCAACATCAACACTACTTACCTCACTGCTGCTATTGATGCTAAGACAGATCCCT 703
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 700 AGTGTCCCATTTTCGACTAGGACATCTTCCGAGAAACAGCGGATTAATTTTCAGATG 759
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 704 TCTGCCCCATATTCGCTTGGCAAAATAGTGGAGAACGACAGGACAGATTTCCAGGACA 763
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 760 KGCATATCAGGGGGAATATGGCATTGAGTCTACTGAGTGCACACCTTAGACCCGT 819
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 764 TGGCCGTGGAGGAGGATCATGGGATCCAGGTCACTGGGACTGCAACCTGGACAGAG 823
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 820 GGTTCATCACTGCCCTCCCAATATAGTTTCCRTCGCTTGAGCAGACAGACCAACAG 879
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 824 CCGCTTCCCTCTGCTTCCAGGTACTCTTCCCGCGCTCGATACACGGGAGTGTGAGC 883
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 880 TGTCTTTGACCTTGGCTTACACTTCAGATACGCCAATACTACAGGAAACAATG--- 936
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 884 ACAACGTATCTCTGCTTACAATTTACAGTTTGGCAAGTACTACAGAGACCTGGCTGGCA 943
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 937 TTGAGAAAGGACTCTGATAAAGTCTTCGGGATCCGTTTGCATCTCTGTTTGTGCA 996
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 944 ACAGAGCGGCACGTCATCAAGSCCTATGSCATCCGCTTCGACATCATTTGTTTGGGA 1003
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
QY 997 CCGAGGAAATTTGACATTTATCCAGCTGGTGTGTATACATCGGCTCAACCCCTCTCTACT 1056
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1004 AGGCAGGAAATTTGACATCATCCCACTACTATGATCAACATCGGCTCTGSCCTGGCATGC 1063
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1057 TCGGTCGTGGCCCTGTGTTCATCGACTTCCCTCATC 1091
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1064 TAGGCATGGCAGCGGTGTGTGTGACATCATAGTC 1098
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
US-09-969-347-225
; Sequence 225, Application US/09969347
; Patent No. US20020115085A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sig
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-69
; CURRENT APPLICATION NUMBER: US/09/969,347
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,598
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,604
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 318
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 225
; LENGTH: 2633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-347-225

Query Match      11.0%; Score 203.8; DB 11; Length 2633;
Best Local Similarity 54.8%; Pred. No. 2.4e-53;
Matches 447; Conservative 5; Mismatches 342; Indels 21; Gaps 2;

QY 285 GTCTTTGACACCGCAGACTACACTTCCCTTTGAGGGGAACCTTTCTTCTGTGTGATGACA 344
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 446 GTCTGGGATGTGGTGTGATACGTCTTCCAGCCAGGGGAGCAACTCTTCTGTGTGATG 505
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 345 AACTTTCTCAAAACAGAGGCCAACAGAGCAGCGGTGTGTCCCGAGTATCCCAACCGCAGG 404
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 506 ACCAATTTTCATCGTGACCCCGGAGCAGACTCAAGGCTACTGCGCAGAGCACCCAGAGGG 565
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 405 AGCTCTCTCTCTGACCGAGTGTAAAGAGATGGATGACCCCGCAGAGCAAGGA 464
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 566 GGCATATCAAGGAAGACAGTGGCTGTACCCCTGGGAGGCCAAGAGGAGGCCCAAGGC 625
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 465 ATTCAGACCGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 524
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 626 ATCCGACGCGCAAGTGTGTGGCTTCAACGACACTGTGAAGACGTGTGAGATCTTTGGC 685
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 525 TGGTCCCATCTGAGGAGTGTGAAGAGGCCCCCGGCTGCTCTCTTGAACAGTCCGAA 584
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 686 TGTGCCCCGTGGAGTGTGATGACATCCCGGCGCTTCTCCGAGAGGCGGAG 745
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 585 AACTTCACTGTCTCATCAAGAACATATCGACTTCCCGGCGCCACAACTACACACGAGA 644
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 746 AACTTCACTCTTTTCATCAGAACAGCATCAGCTTTCCAGCTTCAAGTCAACAGGCGC 805
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 645 AACATCTCTCCAGGTTTAA-----CATCATTGTACCTTCCACAGACTCAG 692
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 806 AACCTGTGTGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 865
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 693 AATCCAGAGTGTCCATTTTCCGACTAGAGACATCTTCGAGAAACAGAGGAGTATTTT 752
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 866 CACCCCTCTCCAGTCTTCCAGCTTGTGCTACGTGTGTGTGTGTGTGTGTGTGTGTGTGT 925
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 753 TCAGATGTGCAATTCAGGCGGATATATGGCATTTGAGATCTACTTGGACTGCAACTA 812
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 926 AGCACCTTGGCTGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 985
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 6
US-09-977-221-3
; Sequence 3, Application US/09977221
; Publication No. US20030008293A1
; GENERAL INFORMATION:
; APPLICANT: MORTEN, JOHN EDWARD NORRIS
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; FILE REFERENCE: PLS/009901/0283779
; CURRENT APPLICATION NUMBER: US/09/977,221
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/244,897

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; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: GB 0025859.0
; PRIOR FILING DATE: 2000-10-21
; PRIOR APPLICATION NUMBER: GB 0108654.5
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO.3
; LENGTH: 11270
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5554)..(5569)
; OTHER INFORMATION: This range may encompass 3 or 4 gttt repeats
US-09-977-221-3

Query Match          7.7%; Score 142.6; DB 12; Length 11270;
Best Local Similarity 97.9%; Pred. No. 1.4e-33;
Matches 142; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      766  TTCAGGGCGGAATAATGGCAATTGAGATCTACTGGACTGCAACCTAGACCGTTGGTTCC 825
Db      7012  TTCAGGGCGGAATAATGGCAATTGAGATCTACTGGACTGCAACCTAGACCGTTGGTTCC 7071

QY      836  ATCACTGCCTCCCAAATACAGTTTCCTCGCCTTGAGCAAGACCAACACGCTGTGCT 885
Db      7072  ATCACTGCCTCCCAAATACAGTTTCCTCGCCTTGAGCAAGACCAACACGCTGTGCT 7131

QY      886  TGTACCTGCTACAACTTCAGATA 910
Db      7132  TGTACCTGCTACAACTTCAGATA 7156

RESULT 7
US-09-918-995-31290
; Sequence 31290, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31290
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(515)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31290

Query Match          6.1%; Score 113.6; DB 12; Length 515;
Best Local Similarity 88.8%; Pred. No. 3.6e-25;
Matches 135; Conservative 0; Mismatches 14; Indels 3; Gaps 1;

QY      5    CGCAGGAGGGAGGCTGTACCATCGCGGCGCTGCTGCAGCTGCAGTCATGTTTCCAGTA 64
Db      151  CGCAGGAAGGGAGGCTGTAAACCGTGCAGCGCTGCTGCAGCTGCAGTCATGTTTCCGTGA 210

QY      65  TGAGACGAACAAGTCACCTGGATCCAGAGCATGAATATGGACACCATTAAGTGGTCTT 124
Db      211  TGAGACAACAAGTCGCGCGGATCCAAAGCATCAATATATGGACACCATTA 267

QY      125  CCAGTGATCATCTTTTCTCCTACGTTTGCCTTT 156

```



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; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11220
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB3058-028-Q1-K1-D8
US-09-960-352-11220

Query Match          4.8%; Score 90.8; DB 11; Length 276;
Best Local Similarity 57.8%; Pred. No. 4.3e-18;
Matches 158; Conservative 2; Mismatches 114; Indels 0; Gaps 0;

QY 665 CATCACTGTACCTCCACAAGACTCAGATCCCACTGTCCTCCATTTCCGACTAGGAGA 724
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 CAAAACGTGCTATTATGATGCGAAAACAGATCCCTTCTGCCCATATTCGACTGGCAA 62

QY 725 CATCTTCGGAGAACAGGCGATAATTTTCAGATGKGGCAATTCAGGGGGGAATAATGG 784
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 AATTGTGGAAGGCGAGGCGACAGCTTCCAGGACATAGCAATTCAGGGAGGAGCATATGG 122

QY 785 CATTCAGATCTACTGGAGCTCAACTAGACCGTTGTTCCATCCTGCTCCCAATA 844
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 CATCCAGATCACTGAGTCACTGCACTGGACAGGCGCGCTCTCTGCTGCGCCAGGTA 182

QY 845 CAGTTTCCTCGCTTGACGACGACCAAGCAACGATGCTGCTACCTGCTGCTACAATT 904
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 183 TTCTTCGCGCGCTGACACACCGTGACTTGGCCACAGTATCCCAAGGCTACAATT 242

QY 905 CAGATAGCCCACTACTACAGGAAACAATGTT 938
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 243 CAGGTTTGCCAACTACTACAGGCGACCTGAAGGTT 276

RESULT 11
US-10-027-632-103774
; Sequence 103774, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 698
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-103774

Query Match          4.8%; Score 89.8; DB 15; Length 698;
Best Local Similarity 96.8%; Pred. No. 1.5e-17;
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1759 GGAAGAGATTCCRAAGAGTGAAGGCGAGTACAGTGGCTTCAAGAGTCTTACTGAAGCC 1818
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GGAAGAGATTCCRAAGAGTGAAGGCGAGTACAGTGGCTTCAAGAGTCTTACTGAAGCC 60

QY 1819 AGGCACCGTGGCTCAGTCTGTATTAATCCACCTTTT 1853
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AGGCACCGTGGCTCAGTCTGTATTAATCCACCGCTT 95

RESULT 13
US-09-918-995-5505
; Sequence 5505, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5505
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-5505
```

```
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11220
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB3058-028-Q1-K1-D8
US-09-960-352-11220

Query Match          4.9%; Score 90.8; DB 11; Length 276;
Best Local Similarity 57.7%; Pred. No. 4.3e-18;
Matches 158; Conservative 2; Mismatches 114; Indels 0; Gaps 0;

QY 665 CATCACTGTACCTCCACAAGACTCAGATCCCACTGTCCTCCATTTCCGACTAGGAGA 724
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 CAAAACGTGCTATTATGATGCGAAAACAGATCCCTTCTGCCCATATTCGACTGGCAA 62

QY 725 CATCTTCGGAGAACAGGCGATAATTTTCAGATGKGGCAATTCAGGGGGGAATAATGG 784
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 AATTGTGGAAGGCGAGGCGACAGCTTCCAGGACATAGCAATTCAGGGAGGAGCATATGG 122

QY 785 CATTCAGATCTACTGGAGCTCAACTAGACCGTTGTTCCATCCTGCTCCCAATA 844
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 CATCCAGATCACTGAGTCACTGCACTGGACAGGCGCGCTCTCTGCTGCGCCAGGTA 182

QY 845 CAGTTTCCTCGCTTGACGACGACCAAGCAACGATGCTGCTACCTGCTGCTACAATT 904
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 183 TTCTTCGCGCGCTGACACACCGTGACTTGGCCACAGTATCCCAAGGCTACAATT 242

QY 905 CAGATAGCCCACTACTACAGGAAACAATGTT 938
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 243 CAGGTTTGCCAACTACTACAGGCGACCTGAAGGTT 276

RESULT 11
US-10-027-632-103774
; Sequence 103774, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103774
; LENGTH: 698
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-103774

Query Match          4.8%; Score 89.8; DB 15; Length 698;
Best Local Similarity 96.8%; Pred. No. 1.5e-17;
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1759 GGAAGAGATTCCRAAGAGTGAAGGCGAGTACAGTGGCTTCAAGAGTCTTACTGAAGCC 1818
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GGAAGAGATTCCRAAGAGTGAAGGCGAGTACAGTGGCTTCAAGAGTCTTACTGAAGCC 60

QY 1819 AGGCACCGTGGCTCAGTCTGTATTAATCCACCTTTT 1853
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AGGCACCGTGGCTCAGTCTGTATTAATCCACCGCTT 95

RESULT 13
US-09-918-995-5505
; Sequence 5505, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5505
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-5505
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CDNA library preparation, Kuan Laboratories;
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>


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QY 1745 CCCTGGAGGATCCGGAAAGAGTTTCCRAAGAGTGAAGGCGAGTACAGTGGCTTCAAGAG 1804
Db 1672 CCCTGGAGATCCCGAAAGAGTTTCGAAGAGTGAAGGCGAGTACAGTGGCTTCAAGAG 1731
QY 1805 TCCTTACTGAAGCCAGGACCGTGGCTGCAGTCTGTAATCCACCTTTT 1853
Db 1732 TCCTTACTGAAGCCAGGACCGTGGCTGCAGTCTGTAATCCACCGCTT 1780

RESULT 2
BI861622
LOCUS 603390486f1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5399565 5',
DEFINITION mRNA sequence.
ACCESSION BI861622
VERSION BI861622.1 GI:16002369
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 795)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM12018 row: k column: 22
High quality sequence stop: 772.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5399565"
/clone_lib="NIH_MGC_87"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 176 a 231 c 228 g 160 t
ORIGIN

Query Match 36.4%; Score 675.2; DB 13; Length 795;
Best Local Similarity 97.7%; Pred. No. 3e-171;
Matches 707; Conservative 8; Mismatches 6; Indels 3; Gaps 3;

QY 1116 CGTCCCATATTTATCCCTGGTGCAGTGTCTGACCCGACATTAAGATATGTCTTTT 1235
Db 1 CGCTCCCATATTTATCCCTGGTGCAGTGTCTGACCCGACATTAAGATATGTCTTTT 120
QY 1176 TACAGNAGAGTGGAGTCCATTTGTGGAGCCGACATTAAGATATGTCTTTT 1235
Db 61 TACAGNAGAGTGGAGTCCATTTGTGGAGCCGACATTAAGATATGTCTTTT 120
QY 1236 GTGGATCAATCCCATAGGATGTGTAACACGACGCTACTAGGAGAGTCTCAAGAT 1295
Db 121 GTGGATCAATCCCATAGGATGTGTAACACGACGCTACTAGGAGAGTCTCAAGAT 180
QY 1296 GTCAAGGCCCAAGAGTCCCAAGACCTGTGATGGACTTCACAGATTTGTCCAGGCTGCC 1355
Db 181 GTCAAGGCCCAAGAGTCCCAAGACCTGTGATGGACTTCACAGATTTGTCCAGGCTGCC 240

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QY 1356 CTGGCCCTCATGACACACACCCCGATTCTCTGGACAAACAGAGGAGATACRGCTCTTAGA 1415
Db 241 CTGGCCCTCATGACACACACCCCGATTCTCTGGACAAACAGAGGAGATACRGCTCTTAGA 300
QY 1416 AAGGAGGCGACTCTCTAGATATCCAGGATAGCCCTGTCTGGTGCAGTGTGGAAGTGCCTC 1475
Db 301 AAGGAGGCGACTCTCTAGATATCCAGGATAGCCCTGTCTGGTGCAGTGTGGAAGTGCCTC 359
QY 1476 CCATCTCAACTCCCTGAGAGCCACAGGTGCTGGAGGAGCTGTGCTGCCGGAAGAGCGG 1535
Db 360 CCATCTCAACTCCCTGAGAGCCACAGGTGCTGGAGGAGCTGTGCTGCCGGAAGAGCGG 419
QY 1536 GGGGCTGTGATCAACACCTCAGAGCTCTTCCAGAACTGTCTCTCCAGACAGTCTCTG 1595
Db 420 GGGGCTGTGATCAACACCTCAGAGCTCTTCCAGAACTGTCTCTCCAGACAGTCTCTG 479
QY 1596 CAGTTCTCTCTCTCTACAGGAGCCCTTGTCTGCGCTGGATGTGATTCACCAACAGC 1655
Db 480 CAGTTCTCTCTCTCTACAGGAGCCCTTGTCTGCGCTGGATGTGATTCACCAACAGC 539
QY 1656 CGGCTGGGCGACTGTGCTCTACAGTGTGACGCACTGCGCTCGGCTCGGCTCCAGAGCATG 1715
Db 540 CGGCTGGGCGACTGTGCTCTACAGTGTGACGCACTGCGCTCGGCTCGGCTCCAGAGCATG 599
QY 1716 GCTGAC-TTTGGCATCTTCCGCGCTGCTGCGCTGGAGATCCGGAAGAGTTTCCGAA 1774
Db 600 GCTGAC-TTTGGCATCTTCCGCGCTGCTGCGCTGGAGATCCGGAAGAGTTTCCGAA 659
QY 1775 GAGTGAAGGCGAGTACAGTGTCTCAAGAGTCC-TTACTGAAGCCAGCCAGCCGCTGCTCA 1833
Db 660 GAGTGAAGGCGAGTACAGTGTCTCAAGAGTCC-TTACTGAAGCCAGCCAGCCGCTGCTCA 719
QY 1834 CGTC 1837
Db 720 CGTC 723

RESULT 3
BF347747
LOCUS 602022588f1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158189
DEFINITION 5', mRNA sequence.
ACCESSION BF347747
VERSION BF347747.1 GI:11295342
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM9433 row: o column: 22
High quality sequence stop: 706.
Location/Qualifiers
1..946
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/db_xref="taxon:9606"
/clone="IMAGE:4158189"
/clone_lib="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"

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421 ACCGAGTGTAAAGAGGATGGATGACCCGACAGAAAGAAATTCAGACCGAAGT 480
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469 ACCGAGGTGTAAAGAGGATGGATGACCCGACAGAAAGAAATTCAGACCGAAGT 528
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481 GTGTAGTATGAGAGGAAACAGAAAGACCTGTGAAGTCTCTGCTGGTCCCATCGAGG 540
|||||
529 GTGTAGTATGAGAGGAAACAGAAAGACCTGTGAAGTCTCTGCTGGTCCCATCGAGG 588
|||||
541 CAGTGAAGAGGCCCCCGGCTGCTCTTGAACAGTGGCGAAATTCACGTGCTCA 600
|||||
589 CAGTGAAGAGGCCCCCGGCTGCTCTTGAACAGTGGCGAAATTCACGTGCTCA 648
|||||
601 TCAAGAACAA-TATCGACTTCCCGGCCCAACTACACACAGAG-AAACATCTCTCCAGG 658
|||||
649 TCAAGAACAA-TATCGACTTCCCGGCCCAACTACACACAGAG-AAACATCTCTCCAGG 708
|||||
659 TTTAAACATCACTGTACCTTCCACAGACTCAGAAATCCACAGTGTCCCATTTCCG-AC 717
|||||
709 TTTAAACATCAANTGTACATTCACAGAAATCCAGATCCAGTGTCCCATTTCCGAAAC 768
|||||
718 TAGGAGA-CACCTCCGAGAAACA-GGCGATATTTTTCAGATGKGCATTCACGGGGG 775
|||||
769 TAGGAGACCATCTCCGAGAAACAGGGGCGAATAATTCAGAAATGTCCCACTTCAGGGGT 828
|||||
776 AATAATGGGCATTGGAGATCTACTGGGACTGCCAAGCTAGACCTAGACCTTGTTCATCACTGCCR 835
|||||
829 GAATATGGGCATTGAATTTACCTGGGACTGGCACTAGACCTGGTTCATCAATGATACA 888
|||||
836 TCCAAATACAGTTTCCTCTGCTTCCGCTTGAACAGCAAGAC 871
|||||
889 TCCAAATACAGTTTCCTCTGCTTCCGCTTGAACAGCAAGACCAAC 924
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RESULT 5
BI603534
LOCUS 603244436F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5286944 5',
DEFINITION mRNA sequence.
ACCESSION BI603534
VERSION BI603534.1 GI:15496473
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11725 row: 9 column: 09
High quality sequence stop: 747.
Location/Qualifiers
1. .932
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/db_xref="taxon:9606"
/clone="IMAGE:5286944"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); site 1: BamHI; site 2: SalI-XhoI (gtcag
); Oligo-dT primed using primer 5'-TTTCTTTTCTTTTCTT-3',

size-selected for average insert size 2.3 kb and
normalized to R01 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 244 a 238 c 247 g 203 t

ORIGIN

Query Match 34.8%; Score 645.4; DB 13; Length 932;
Best Local Similarity 94.1%; Pred. No. 3.8e-163;
Matches 712; Conservative 3; Mismatches 34; Indels 8; Gaps 4;

QY 5 CGCAGGAGGGAGGCTGTCACTCCGATCCAGAGCATGAATATGSCACCATTAAGTGGTTCTT 124
Db |||||
QY 13 CGCAGGAGGGAGGCTGTCACTCCGATCCAGAGCATGAATATGSCACCATTAAGTGGTTCTT 132
Db |||||
QY 65 TGAGAGCAACAAAGTCACTCCGATCCAGAGCATGAATATGSCACCATTAAGTGGTTCTT 124
Db |||||
QY 73 TGAGAGCAACAAAGTCACTCCGATCCAGAGCATGAATATGSCACCATTAAGTGGTTCTT 132
Db |||||
QY 125 CCACGTGATCATCTTTTCCCTACGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 184
Db |||||
QY 133 CCACGTGATCATCTTTTCCCTACGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 192
Db |||||
QY 185 GAAAGAGCCCTGTCACTCTGTGACACCAAGTGTGAGGGGATGACAGAGTGAAGA 244
Db |||||
QY 193 GAAAGAGCCCTGTCACTCTGTGACACCAAGTGTGAGGGGATGACAGAGTGAAGA 252
Db |||||
QY 245 GGAGATCGYGGAGAAATGAGTGAAGAGTGTGTCACAGTGTCTTTGACACCGCAGACTA 304
Db |||||
QY 253 GGAGATCGYGGAGAAATGAGTGAAGAGTGTGTCACAGTGTCTTTGACACCGCAGACTA 312
Db |||||
QY 305 CACCTTCCCTTTGAGGGGAACTCTTTCTTCTGTAAGTGAAGTGTCTTTCAAAAACAAGG 364
Db |||||
QY 313 CACCTTCCCTTTGAGGGGAACTCTTTCTTCTGTAAGTGAAGTGTCTTTCAAAAACAAGG 372
Db |||||
QY 365 CCAGAGAGCAGCGTGTCTCCGAGTATCCACCCGAGGAGCTCTCTCTCTCTCTCTCTCT 424
Db |||||
QY 373 CCAGAGAGCAGCGTGTCTCCGAGTATCCACCCGAGGAGCTCTCTCTCTCTCTCTCTCT 432
Db |||||
QY 425 AGGTGTGTAAGAGGATGGATGGACCCGACAGACCAAGGAATTCAGACCGGAGGTGTGT 484
Db |||||
QY 433 AGGTGTGTAAGAGGATGGATGGACCCGACAGACCAAGGAATTCAGACCGGAGGTGTGT 492
Db |||||
QY 485 AGTGTATGAAGGAAACCAAGAGACCTGTGAAGTCTCTGCTGTGTCGCCCAATPCGAGGAGT 544
Db |||||
QY 493 AGTGTATGAAGGAAACCAAGAGACCTGTGAAGTCTCTGCTGTGTCGCCCAATPCGAGGAGT 552
Db |||||
QY 545 GGAAGAGGCCCCCGGCTGCT-CTCTTGAACAGTGCAGAAA--CTTCACTGTGCTCAT 601
Db |||||
QY 553 GGAAGAGGCCCCCGGCTGCTCTCTTGAACAGTGCAGAAAATTCACCTGTGCTCAT 612
Db |||||
QY 602 CAAGAAACAATATCGACTTCCCGGCCCAACTACACCCAGAGAAACATPCT--GCCAGGT 659
Db |||||
QY 613 CAAGAAACAATATCGACTTCCCGGCCCAACTACACCCAGAGAAACATPCTTCCCGAGG 672
Db |||||
QY 660 TTAACATCACTTGTACCTTCCACAGACTTCAGAAATPCACA---GTGTCATTTCCGA 716
Db |||||
QY 673 TTTAACAATCACTTGTACCTTCCACAGACTTCAGAAATPCACAAGTGGTCTCAATTTTCCG 732
Db |||||
QY 717 CTAGGAGACATCTCCGAGAAACAGGGCGATAATTTT 753
Db |||||
QY 733 TAAGGAGACATCTTCCCGAGAAACAGGGCGAGTACTT 769
Db |||||

RESULT 6
BI603534
LOCUS 602739207F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4869288 5',
DEFINITION mRNA sequence.
ACCESSION BI603534
VERSION BI603534.1 GI:14077102

KEYWORDS SOURCE ORGANISM

EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 769)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM1740 row: m column: 01
High quality sequence stop: 654.
Location/Qualifiers
1..769
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4869288"
/clone_lib="NIH_MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; site_1: XhoI; site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH-MGC
Library." 198 a 189 c 215 g 167 t

FEATURES source

RESULT 7
BI598073
LOCUS
DEFINITION
860 bp mRNA linear EST 07-SEP-2001
60325308F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5304048 5',
mRNA sequence.
ACCESSION
BI598073
VERSION
BI598073.1 GI:15491012
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 860)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM1769 row: p column: 01
High quality sequence stop: 711.
Location/Qualifiers
1..860
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5304048"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtogag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTN-3',
size-selected for average insert size 2.3 kb and
normalized to 80T 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."
223 a 211 c 239 g 187 t

BASE COUNT ORIGIN

Query Match 33.4%; Score 619.8; DB 12; Length 769;
Best Local Similarity 95.2%; Pred. No. 2.8e-156;
Matches 690; Conservative 3; Mismatches 25; Indels 7; Gaps 5;
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DB 49 CGCAGGAGGAGGCTGTCACCATGCCGCTGTGAGCTGCAGTGAGTGTTCAGTA 108
QY 65 TGAGACGAAACAACTACTCGGATCCAGAGCATGAATATGGACCATTAAGTGTCTT 124
DB 109 TGAGACGAAACAACTACTCGGATCCAGAGCATGAATATGGACCATTAAGTGTCTT 168
QY 125 CCACGTGATCATCTTTCCCTACGTTGCTTGTGTCACACCAAGGTGAAGGATACAGAGCTTACCAGC 184
DB 169 CCACGTGATCATCTTTCCCTACGTTGCTTGTGTCACACCAAGGTGAAGGATACAGAGCTTACCAGC 228
QY 185 GAAGAGGCTGTCTATCATGTTCTGTGCACACCAAGGTGAAGGATACAGAGCTGAAGA 244
DB 229 GAAGAGGCTGTCTATCATGTTCTGTGCACACCAAGGTGAAGGATACAGAGCTGAAGA 288
QY 245 GGAGATCGYGGAGATGAGTGAA-GAAGTTGGTGCACAGTGTCTTTGACACCGCAGACT 303
DB 289 GGAGATCGYGGAGATGAGTGAGGACGTTGGTGCACAGTGTCTTTGACACCGCAGACT 348
QY 304 ACACCTTCCTTCGAGGGGACTCTTTCTGTGATGACAACTTCTCA-AAACAGAA 362
DB 349 ACACCTTCCTTCGAGGGGACTCTTTCTGTGATGACAACTTCTCAAGAACAGAA 408
QY 363 GGCCAAAGACACGGTGTGTGCCGAGTATCCACCGCAGAGGCTGTCTTCCTTCAC 422
DB 409 GGCCAAAGACACGGTGTGTGCCGAGTATCCACCGCAGAGGCTGTCTTCCTTCAC 468
QY 423 CGAGGTTGTAAAAAGGGATGGATGGACCCGACAGACAAAGGAATTCAGACCGGAAGTGT 482

Db 469 CGAGTGTGTAAAAAGGGATGGATGGACCCGACAGACAAAGGAATTCAGACCGGAAGTGT 528
QY 483 GTATGTYATGAAGGAACACAGAGACCTGTGAAGTCTCTGCTGGTGCCTCATCGAGGCA 542
Db 529 GTAGTCATGACGAGGGAACACAGAGAGCTGTGAAGTCTCTGCTGGTGCCTCATCGAGGCA 587
QY 543 GTGGAAGACCCCGCGGCTGCTCTTTGAACAGTGCAGAAACTTCACTGTGCTCATC 602
Db 588 GGG---AAGAGGCCCGCGGCTGCTCTTTGAACAGTGCAGAAACTTCACTGTGCTCATC 644
QY 603 AAGAACAAATATGACTTCCCGGCGCACAACTACACACAGAGAAACATCCTCCAGAGTTTA 662
Db 645 AAGAACAAATATGCTTCCCGGCGCACAAATACACACAGAGAAACATCCTCCAGAGTTTA 704
QY 663 AACATCACTGTGATCC-TTCCCAAGAGTCAAGATCAACAGTGTCCCATTTCCGATGAG 721
Db 705 ACGATCACTGTGATCCGTACAGAGACTCAGAAATCCACAGTGTCCCATTTATCGACTAG 764
QY 722 AGACA 726
Db 765 AGACA 769

FEATURES source

1..860
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/clone="IMAGE:5304048"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtogag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTN-3',
size-selected for average insert size 2.3 kb and
normalized to 80T 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."
223 a 211 c 239 g 187 t

Query Match 30.4%; Score 564; DB 13; Length 860;

[illegible]

Dib 2

[illegible]


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QY 1752 AGGATCCGGAAGAGTTTCRAAGAGTGAAGGCGAGTACAGTGGCTTCAGAGTCCCTTAC 1811
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295 AGATCCGGAAGAGTTTCGAAGAGTGAAGGCGAGTACAGTGGCTTCAGAGTCCCTTAC 236
QY 1812 TGAAGCCAGGACCGTGGCTCAAGTCTGTAATCCCACTTTT 1853
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
235 TGAAGCCAGGACCGTGGCTCAAGTCTGTAATCCCACTTTT 194

RESULT 12
BF347290
LOCUS BF347290 543 bp mRNA linear EST 22-NOV-2000
DEFINITION 602021043F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156427
5' mRNA sequence.
ACCESSION BF347290
VERSION BF347290.1 GI:11294885
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 543)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA library Preparation: Life Technologies, Inc.
DNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM9429 row: f column: 12
High quality sequence stop: 543.
FEATURES
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1..543
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4156427"
/collection="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: Brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.3 Kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 148 a 122 c 155 g 118 t
ORIGIN
Query Match 23.2%; Score 430; DB 12; Length 543;
Best Local Similarity 98.9%; Pred. No. 4.7e-105;
Matches 463; Conservative 1; Mismatches 1; Indels 3; Gaps 3;
QY 5 CGCAGGAGGAGGAGTGTCCATCGCGGCTGCTGCAGCTGCAGTGCAGTGTTCACGTA 64
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 CGCAGGAGGAGGAGTGTCCATCGCGGCTGCTGCAGCTGCAGTGCAGTGTTCACGTA 108
QY 65 TGAGACGAACAAGTCACTCGGATCCAGACATGAATTATGGCACCATTAAAGTGTCTT 124
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
109 TGAGACGAACAAGTCACTCGGATCCAGACATGAATTATGGCACCATTAAAGTGTCTT 168
QY 125 CCACGTCATCCTTTTCTACGTTTCTTCTCTGCTGAGTGCAGAGCTGTACCAGG 184
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
169 CCACGTCATCCTTTTCTACGTTGCTTCTCTGCTGAGTGCAGAGCTGTACCAGG 227
QY 185 GAAAGAGCCTGTATCATCTCTGTGCACACCAAGTGAAGGGATACAGAGTGAAGA 244
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
228 GAAAGAGCCTGTATCATCTCTGTGCACACCAAGTGAAGGGATACAGAGTGAAGA 287
QY 245 GGAGATCGYGGAGAATGAGTGAAGAAGTGTGGTGCACAGTGTCTTTGACACCGCAGACTA 304

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Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
288 GGAGATCGTGGAGATGGAGTGAAGAAGTGTGTCACAGTGTCTTGCACCGCAGACTA 346
QY 305 CACCTTCCCTTTTCAGGGGAACCTTTTCTGCTGATGACAACTTTCTCAAAACAGAAG 364
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
347 CACCTTCCCTTTTCAGGGGAACCTTTTCTGCTGATGACAACTTTCTCAAAACAGAAG 405
QY 365 CCAAGAGCAGCGTTGTGTCGCGAGTATCCCAACCGCAGGACGCTGTCTCTGACCG 424
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
406 CCAAGAGCAGCGTTGTGTCGCGAGTATCCCAACCGCAGGACGCTGTCTCTGACCG 465
QY 425 AGTGTGTAAGAGGATGGATGACCCGACAGCAAAAGGAATTCAGAC 472
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
466 AGTGTGTAAGAGGATGGATGACCCGACAGCAAAAGGAATTCAGAC 513

RESULT 13
BF554327
LOCUS BF554327 642 bp mRNA linear EST 20-JUN-2002
DEFINITION H4027E01-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
5' mRNA sequence.
ACCESSION BF554327
VERSION BF554327.1 GI:21455215
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 642)
AUTHORS VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin
P.R., Stagg,C.A., Bassey,U., Aiba,K., Hamatani,T., Kargul,G.J.,
Luo,A.G. and KO,M.S.H.
TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse
cDNA clone set
JOURNAL Unpublished (2002)
COMMENT Other_ESTs: H4027E01-3
Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdnaelg@nigms.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7.4K.html for details.
Seq primer: -21M13 Reverse
High quality sequence stop: 642
POLYA=No.
FEATURES
source
1..642
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="niaEST:H4027E01-5"
/db_xref="taxon:10090"
/clone_lib="NIA Mouse 7.4K cDNA Clone Set"
/sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
/notes="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
clone is among a rearrayed set of 7,407 clones from more
than 20 cDNA libraries."
BASE COUNT 133 a 199 c 179 g 131 t
ORIGIN
Query Match 21.6%; Score 400.8; DB 14; Length 642;
Best Local Similarity 80.2%; Pred. No. 4.1e-97;
Matches 465; Conservative 4; Mismatches 111; Indels 0; Gaps 0;
QY 1242 GAATCCCATTTAGGATGGTGAACAGCAGCTACTAGGAGAAAGTGTGCAAGATGTCAAG 1301
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 GAGCCGCACATTCGATGGTGGACAGCAGCTGCTGGGAAAGTGTGCAATTTCTCAA 60
QY 1302 GGCCAAGAAGTCCSAAGACCTGTGATGGACTTCAAGATTTGCCAGGCTGCCCTGSCC 1361

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: L1AM9429 row: g column: 13
High quality sequence start: 39
High quality sequence stop: 541.

FEATURES

SOURCE

1..555
Location/Qualifiers
loss"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4156452"
/clone_lib="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with 1p/19q loss"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 144 a 134 c 154 g 123 t
ORIGIN

Query Match 20.1%; Score 373; DB 12; Length 555;
Best Local Similarity 95.8%; Pred. NO. 1.2e-89;
Matches 457; Conservative 1; Mismatches 11; Indels 8; Gaps 7;
QY 6 GCAGGAGGAGGCTGCACCATGCCGCCCTGTCAGCTGCAGTGAAGTTTCCAGTAT 65
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
52 GCAGGAGGAGGCTGCACCATGCCGCCCTGTCAGCTGCAGTGAAGTTTCCAGTAT 110
QY 66 GAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAAGTGGTTCTC 125
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
111 GAGACGAACAAAGTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAAGTGGTTCTC 170
QY 126 CACGTGATCATCTTTTCCTAC--GTTTCTTGTCTCTGTTGAGTGAACAAGCTGT-ACCAG 182
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
171 CACGTGATCATCTTTTCCTAC--GTTTCTTGTCTCTGTTGAGTGAACAAGCTGTCAACAG 230
QY 183 CGGAAGAGCTGTCACTGTCAGTCTGTGCACACCAAGCTGAAGGGGATACGAGAGTGAAA 242
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
231 CGGAAGAGCTGTCACTGTCAGTCTGTGCACACCAAGCTGAAGGGGATACGAGAGTGAAA 290
QY 243 GAGGAGATCGYGGG-GAATGGAGTGAAGAAGTTGTCACAGTGTCTTTGACACCGCAGA 301
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
291 GAGGAGATCGTGGACGAATGGAGTGAAGAAGTTGTCACAGTGTCTTTGACACCGCAGA 350
QY 302 CTACACCTTCCCTTTTCAGGGGACTCTTCTTCTGTTGATGACAAACTTTCTCAAAACAGA 361
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
351 CTACACCTTCCCTTTTCAGGGGAACTCTTCTTCTGTTGATGACAAACTTTCTCAAAACAGA 410
QY 362 AGGCCAAGACGAGCGGTTGTGCCGAGTATCCACCGCAGGACGCTGTGTCCTCTGA 421
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
411 AGGCCAAGACGAGCGGTTGTGCCGAGTATCCCA-CCGACGACGCTGTGTCCTCTGA 469
QY 422 CCGAGGTTGTA-AAAGGATGATGG-ACCGCAGACCAAGAAATTCAGACCGGA 476
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
470 CCGAGGTTGTACACAGGATGCTGGCACCACCGCAGACCAAGAAATTCAGACCGGA 526

Search completed: July 18, 2003, 19:00:05
Job time : 2721 secs